

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 14:16:48 ; Search time 43 Seconds
(without alignments)
443.045 Million cell updates/sec

Title: US-09-647-544-2_COPY_140_337
Perfect score: 1025
Sequence: 1 GICARVDASFPQGS LAPTA.....FLRIRTIASDPDERFFNV 198

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 100665

Minimum DB seq length: 0
Maximum DB seq length: 198

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: Pirl:.*
2: pirl2:.*
3: pirl3:.*
4: pirl4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	336	32.8	191	2	VLA-2 protein - pi
2	74	7.2	194	2	beta 8 integrin -
3	71	6.9	164	2	hypothetical prote
4	71	6.9	169	2	hypothetical prote
5	71	6.9	170	2	complement C4 - ch
6	71	6.9	197	2	hypothetical prote
7	70.5	6.9	118	2	hypothetical prote
8	70	6.8	188	2	transcription regu
9	69.5	6.8	148	2	conserved hypotet
10	69	6.7	129	2	hypothetical prote
11	68.5	6.7	148	2	acetyltransferase,
12	68	6.6	171	2	hypothetical prote
13	67.5	6.6	151	2	hypothetical prote
14	67.5	6.6	193	2	Jag-related protei
15	67	6.5	181	2	hypothetical prote
16	67	6.5	197	2	rubrerythrin - Met
17	66.5	6.5	166	2	30S ribosomal prot
18	66.5	6.5	187	2	acetyl transferase
19	66	6.4	138	2	virulence regulato
20	66	6.4	180	2	conserved hypotet
21	65.5	6.4	147	2	Ni,Fe-Hydrogenase
22	65	6.3	86	1	gonadolibirin II p
23	65	6.3	170	2	complement C4 - go
24	65	6.3	189	2	hypothetical prote
25	65	6.3	196	2	acetyltransferase
26	64.5	6.3	190	2	hypothetical prote
27	64	6.2	129	2	hypothetical prote
28	64	6.2	129	2	IS426 transposase
29	64	6.2	129	2	IS 426 transposase

30	64	6.2	131	2	JC7739	paralytic peptide
31	64	6.2	157	2	T30772	hypothetical prote
32	63.5	6.2	85	2	A53453	gonadolibirin II p
33	63.5	6.2	178	2	AH1330	hypothetical prote
34	63	6.1	194	2	H89940	conserved hypotet
35	62.5	6.1	108	2	B75029	hypothetical prote
36	62.5	6.1	178	2	AH1701	hypothetical prote
37	62	6.0	161	1	A30477	hemoglobin VIIIB-6
38	62	6.0	161	1	S04499	hemoglobin VIIIB-8
39	62	6.0	193	2	T32808	hypothetical prote
40	61.5	6.0	164	2	D84286	hypothetical prote
41	61.5	6.0	180	2	D83623	hypothetical prote
42	61.5	6.0	182	2	B56274	sulfur-regulated p
43	61	6.0	102	2	D84397	hypothetical prote
44	61	6.0	161	1	JT0232	hemoglobin VIIIB-5
45	61	6.0	161	1	JT0349	hemoglobin VIIIB-5

ALIGNMENTS

RESULT 1

I47230
VLA-2 protein - pig (fragment)
N:Alternate names: glycoprotein Ia/IIa
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I47230; S21518
R:Bahou, W.F.; Potter, C.L.; Mirza, H.
Blood 84, 3734-3741, 1994
A:Title: The VLA-2 (alpha 2 beta 1) I domain functions as a ligand-specific recognition
A:Reference number: I47230; MUID:95036279; PMID:7949129
A:Accession: I47230
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-191 <BAH>
A:Cross-references: UNIPROT:Q29124; EMBL:Z12137; NID:g2158; PIDN:CAA78125.1; PID:g2159
C:Keywords: Glycoprotein

Query Match	32.8%;	Score	336;	DB	2;	Length	191;
Best Local Similarity	43.9%;	Pred. No.	1.9e-23;				
Matches	69;	Conservative	27;	Mismatches	61;	Indels	0;
Gaps	0;						
Qy	42	WSEVQTFLRLVGLFIDPEIQVGLVQYQESPVHWSLGDFTKKEEVVRAAKNLSRREG	101				
Db	1	WDAYKNFLKRVQGLDIGPTKTQVGLIQYANNRPWFNLNFTKTKAEMVEATSHTTQYGG	60				
Qy	102	RETQTQAQIMVACTEGFSQSHGGRPEARLLVVVTDGESHDELPALKACEAGRVTTRY	161				
Db	61	DLTWTFAIQYARDSAYSAAAGRGATKVMVVVTDGESHGSMKKAVIDOCNNDNIURF	120				
Qy	162	GIAVLGHLRRQRDPSSFLREIRTIASDPDERFFNV	198				
Db	121	GIAVLGVLNRLDNLTKNLKEIKAIASIPTEYFNV	157				

RESULT 2

I51310
beta 8 integrin - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C:Accession: I51310
R:Venstrom, K.; Reichardt, L.
Mol. Biol. Cell 6, 419-431, 1995
A:Title: Beta 8 integrins mediate interactions of chick sensory neurons with laminin-1,
A:Reference number: I51310; MUID:95352850; PMID:7542940
A:Accession: I51310
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-194 <VEN>
A:Cross-references: UNIPROT:Q91415; GB:S78729; NID:g1042047; PIDN:AAB34966.1; PID:g10420
C:Superfamily: integrin beta chain; laminin-type EGF-like homology

Query Match	6.8%;	Score 70;	DB 2;	Length 188;
Best Local Similarity	25.0%;	Pred. No. 48;		

Query M
Best Lo
Matches

Query Match 6.7%; Score 69; DB 2; Length 129;
Best Local Similarity 23.0%; Pred. No. 38;
Matches 29; Conservative 19; Mismatches 50; Indels 28; Gaps 5;
Qy 12 PGSLAPTAOR-----CPTYMDVIVLDCGNSIYPWSEVQTFELRLVGLKFLIDPQIQ 64

Db 17 PAG--AAVARRLRGSTVHAPAHFV-----EVYGAIRQAVVRQLSDHEGL 60
Qy 65 VGLVOYGSPVHWSLGDFTKKEVWRAAKNLSRRREGRTKTAQAI---MVACTEGFSQS 121
Db 61 VVVNFLSLPVRWPLKPTQORAYQLRSTHTVA--DGAYVALAEGLGVPLITCDGRLAQS 118
Qy 122 HGRPE 127
Db 119 HGHNAE 124

RESULT 11
G95210
acetyltransferase, GNAT family [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
C:Accession: G95210
R:Tattelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapf
neon, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95210
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <KUR>
A:Cross-references: UNIPROT:Q97P37; GB:AE005672; PIDN:AAK75880.1; PID:G14973306; GSPDB:G
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: SPI807

Query Match 6.7%; Score 68.5; DB 2; Length 148;
Best Local Similarity 25.0%; Pred. No. 50;
Matches 28; Conservative 25; Mismatches 34; Indels 25; Gaps 6;

Qy 9 SFQPGSLAPTAQRCPTMYDVIVLDGNSIYPSWSEVQTFLRRL-----VGKLFIDP 60
Db 27 SFQEQW-MGP---RIP-FLTLQLAELGVFSIFDQEFVGFQIKRLSDSNLHGRFFINP 81

Qy 61 EQIQVGLVOYGSPVHWSLGDFTK-----EVVRAAKNLSRRREGRE 103
Db 82 QKQEGGL---GSKALRKFSVSLAFENRDLSDISLVNFEANQRAQNLQKEGFE 130

RESULT 12
H75017
hypothetical protein PAB1243 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H75017
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A:Reference number: A75001
A:Accession: H75017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-171 <KAW>
A:Cross-references: UNIPROT:Q9UY30; GB:AJ248288; GB:AL096836; NID:G5458960; PIDN:CAB5058
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB1243

Query Match 6.6%; Score 68; DB 2; Length 171;
Best Local Similarity 24.3%; Pred. NO. 65;
Matches 33; Conservative 17; Mismatches 44; Indels 42; Gaps 6;

Qy 40 YPMSEVQTFLLRLVGLKFLIDPEQIQVGLVOYGESP-----VHWSLGDGPF----- 83
Db 52 YS1HSSAMKVLG-----VGLVQRIKPGDRRAYFVATKPNFSEWRSAFYEKI 101

Qy 84 -----RTKEEVWRAAKNLSRRREGRTKTAQAINVACTEGFSQSHGGRPEAAR-LLVVVTD 137
Db 102 LRDIETKESIMRALEELGEQSGSEVEIEKELKMLAR-----RNEVARKULTLIMQ 153
Qy 138 GESHGDEELPAALKAC 153
Db 154 FKSE--BELLKVLESC 167

RESULT 13
AF2520
hypothetical protein alr7342 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alr
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C:Accession: AF2520
R:kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AF2520
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <KUR>
A:Cross-references: UNIPROT:Q8YKP6; GB:BA000020; PIDN:BA877100.1; PID:G17134541; GSPDB:G
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr7342
A:Genome: plasmid

Query Match 6.6%; Score 67.5; DB 2; Length 151;
Best Local Similarity 26.9%; Pred. No. 63;
Matches 14; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

Qy 50 RRLVGLKFLIDPEQIQVGLVOYGSPVH-EWSLGDFTKKEVWRAAKNLSRE 100
Db 95 KRLVAEVFNVRNSVNLTMVQEGQAVVRYVLYKGYTNTKEQFLQAEANAKQOK 146

RESULT 14
E75544
Jag-related protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: E75544
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: E75544
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-193 <WHI>
A:Cross-references: UNIPROT:Q9RXR1; GB:AE001886; GB:AE000513; NID:G6457921; PIDN:AAF0983
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0246
A:Map position: 1

Query Match 6.6%; Score 67.5; DB 2; Length 193;
Best Local Similarity 24.5%; Pred. No. 84;
Matches 40; Conservative 22; Mismatches 50; Indels 51; Gaps 9;

Qy 13 QGSLAPTAQRCPTMYDVIVLDGNSIYPSWSEVQTFLRLVGLKFLIDPE-QIQVGLVOYG 71
Db 21 ESALPPPA---PDAAPVSAFLHGADE-DPRAVLEQFLAELTAR-IDPGLRVQV----- 68

Qy 72 ESPVHWSLGDFTKKEVWRA---AKNLSRRREGRTKTAQAINVACTEGFSQSHGGRPE- 127
Db 69 -----RETEDALEAEISGENAARLAGRDGRTLGAIEVIAVAVLAK-HAGRGDL 115

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OM protein - protein search, using sw model

Run on: April 6, 2005, 14:28:38 ; Search time 184 Seconds
(without alignments)
551.042 Million cell updates/sec

Title: US-09-647-544-2_COPY_140_337
Perfect score: 1025
Sequence: 1 GICARVDASFPQGS LAPTA.....FLREIRTIASDPDERFFNV 198

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 646258

Minimum DB seq length: 0
Maximum DB seq length: 198

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	336	32.8	191	2	Q29124 sus scrofa
2	299	29.2	156	2	Q1V33 homo sapien
3	103.5	10.1	143	2	Q7J73 bos taurus
4	92	9.0	146	2	O96930 plasmodium
5	80.5	7.9	153	2	Q8MVN3 boltenia vi
6	79.5	7.8	174	2	Q7AL73 lactobacill
7	79.5	7.8	179	1	FLA1_PLAAC
8	74.5	7.3	181	2	Q8Z280
9	74	7.2	194	2	Q91415 gallus gall
10	73	7.1	196	2	Q821E5
11	72.5	7.1	134	2	Q920X7
12	72.5	7.1	184	2	Q63LC8
13	72.5	7.1	184	2	Q83YN4
14	72.5	7.1	185	2	Q8KYU9
15	72.5	7.1	187	2	Q8Q4X1
16	72	7.0	156	2	Q894X1 clostridium
17	72	7.0	173	2	Q8Z7U4
18	72	7.0	197	2	Q8LD28
19	71.5	7.0	108	2	Q8TWC9 methanopyru
20	71.5	7.0	151	2	Q84670
21	71	6.9	145	2	Q72BK3 desulfovibr
22	71	6.9	164	2	Q8RS46 deinococcus
23	71	6.9	169	2	Q8S027
24	71	6.9	170	2	Q82786
25	71	6.9	174	2	Q9X957
26	71	6.9	197	2	Q9M0V0
27	70.5	6.9	118	2	Q8Z448
28	70.5	6.9	118	2	Q8ZME3 salmonella
29	70.5	6.9	142	2	Q6T825
30	70.5	6.9	166	2	Q7NP32
31	70.5	6.9	198	2	Q7RYR1

32	70	6.8	152	2	Q8MVP6
33	70	6.8	188	2	Q8YHB1
34	70	6.8	188	2	Q8GOK2
35	69.5	6.8	119	2	Q7XHY1
36	69.5	6.8	148	2	Q8DNN2
37	69	6.7	129	2	P71978
38	69	6.7	129	2	P71978 mycobacteri
39	69	6.7	129	2	Q7TZ04
40	68.5	6.7	127	2	Q82N64
41	68.5	6.7	148	2	Q728S1
42	68.5	6.7	163	2	Q9HPQ1
43	68.5	6.7	168	2	Q8PZ58
44	68	6.6	122	2	Q6Z8A2
45	68	6.6	133	2	Q98J17

ALIGNMENTS

RESULT 1

Q29124 ID Q29124 PRELIMINARY; PRT; 191 AA.
AC Q29124;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE VLA-2 (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endothelial;
RX MEDLINE=95036279; PubMed=7949129;
RA Bahou W.F., Potter C.L., Mirza H.;
RT "The VLA-2, (alpha 2 beta 1) I domain functions as a ligand-specific
RT recognition sequence for endothelial cell attachment and spreading:
RL molecular and functional characterization.";
RL Blood 84:3734-3741(1994).
DR EMBL; Z12137; CAA78125.1; -.
DR PIR; I47230; I47230.
DR HSP; P17301; IAOX.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00234; VWA; 1.
FT NON_TER 1 191
FT NON_TER 191 191
SQ SEQUENCE 191 AA; 20896 MW; 2E228B472EC699D8 CRC64;

Query Match 32.8%; Score 336; DB 2; Length 191;

Best Local Similarity 43.9%; Pred No. 1e-21; Indels 0; Gaps 0;
Matches 69; Conservative 27; Mismatches 61;

Qy	42	WSEVQTFLRLVGLFIDPEIQVGLVQYGSPVHWSLGDFTKEEVVRAAKNLSRREG	101
Db	1	WDAVKNLEKRVQGLDIGPTKTVGLIQYANNPRVFNLTFTKAEVVEATSHTYGG	60
Qy	102	REYTKAQAIWVACTEGFSQSHGRPEARLLVVVTDSHDSGELPALKAKACEAGRVTY	161
Db	61	DLTNTFKAIQVARDAYSAAAGRGPGATKVVVVVTDGSHDGLKAVIDQCNDNLRF	120
Qy	162	GIAVLGHVLRQRDPSSFLREIRTIASDPDERFFNV	198
Db	121	GIAVLGLYNRLDNLTKNLKEIKAIASIPTEYFFNV	157

RESULT 2

Q71V33 ID Q71V33 PRELIMINARY; PRT; 156 AA.
AC Q71V33;

```
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Integrin alpha 2 (Fragment).
GN Name=ITGA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kunicki T.J., Krizsik M.R.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF035968; AAC94975.1; -.
DR HSBP; P17301; IAOX.
DR GO; GO:0007229; P:integrin-mediated signaling pathway; IEA.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
KW Integrin.
FT NON_TER 1 1
FT NON_TER 156 156
SQ SEQUENCE 156 AA; 17042 MW; BC7ABD63226C652B CRC64;

Query Match 29.2%; Score 299; DB 2; Length 156;
Best Local Similarity 44.1%; Pred. No. 1.5e-18;
Matches 63; Conservative 24; Mismatches 56; Indels 0; Gaps 0;

Qy 56 LFIDPEIQVGLVQGESPVHWSLGDFTKKEVVRRAAKNLSRREGRTKTAQIMVACT 115
Db 3 LDIGPTKTVGLIQYANNPRVFNLTNYKTKKEIMVATQTSQYGGDLTNTFGAIQYARK 62

Qy 116 EGFSSQSGRGPEARLLVVVTDGSHDGEELPALAKACEAGRVTTRYGIALLVLRQRD 175
Db 63 YAYSAAGGRSRATKVMVWVTDGSHDGMKKAVIDQCNHNDNILRFGIALLVLRNRALD 122

Qy 176 PSSFLREIRTIASDPDERFFENV 198
Db 123 TKNLKEIKAIASIPTRYFFNV 145

RESULT 3
ID Q7J73 PRELIMINARY; PRT; 143 AA.
AC Q7J73;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Von Willebrand Factor (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Porter C.A.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF004285; AAB61376.1; -.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
FT NON_TER 1 1
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16099 MW; D472A917993E1C5A CRC64;

Query Match 10.1%; Score 103.5; DB 2; Length 143;
Best Local Similarity 23.6%; Pred. No. 0.29;
Matches 26; Conservative 27; Mismatches 56; Indels 1; Gaps 1;
```

```
Qy 48 FLRLVGLKFLDPEIQVGLVQGESPVHWSLGDFTKKEVVRRAAKNLSRREGRTKTA 107
Db 14 FVEVIRRMVDVGQDGIHVTVLQYVYVTVVHSHPREPQSKDVVLQRLREVRVYRGNTGTG 73

Qy 108 QAIMVACTEGFSQSHGGRPEARLLVVVTDGSHDG-BELPAALAKACEAG 156
Db 74 LALQYLSEHSFSASQSDREBQAPNLVYVMTGSPASDKIQRMFGDIQLVPIG 123

RESULT 4
O96930 PRELIMINARY; PRT; 146 AA.
AC O96930;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Thrombospondin-related anonymous protein (Fragment).
GN Name=TRAP-2;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA Doering C.D., Doerig C.M.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; X87840; CAA61109.1; -.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS0234; VWFA; 1.
FT NON_TER 1 1
SQ SEQUENCE 146 AA; 16718 MW; A291357664B9F784 CRC64;

Query Match 9.0%; Score 92; DB 2; Length 146;
Best Local Similarity 23.9%; Pred. No. 3.1;
Matches 32; Conservative 29; Mismatches 49; Indels 24; Gaps 6;

Qy 23 CPTYMDVVIVLDGNSI--YPM-SEVQTLRLVGLKFLDPEIQVGL-----VQ 69
Db 11 CQNYDLTLILDESASIGSKNWKSHVIPFTDKIILKDLITKSNKRVHVGILLFSSKNRDYVT 70

Qy 70 YGSPVHWSLGDFTKKEVVRRAAKNLSRRE--GRETCTAQAIAIMVACTEGFSQSHGGRPE 127
Db 71 YGDELRYQ-----KDELLKKVKLKKDYCGGKILGALKYS-LENYTKHKNIRYD 121

Qy 128 AARLLVVVTDGESH 141
Db 122 APKVTILFTDGNEN 135

RESULT 5
O8MVN3 PRELIMINARY; PRT; 153 AA.
AC O8MVN3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Collagen-like protein 3 (Fragment).
GN Name=vwa3;
OS Boltenia villosa.
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Scolidobranchia; Pyuridae; Boltenia.
OX NCBI_TaxID=63515;
RN [1]
RP SEQUENCE FROM N.A.
RA Davidson B.J., Swalla B.J.;
RL MEDLINE=22248966; PubMed=12361966;
RT "A molecular analysis of ascidian metamorphosis reveals activation of an innate immune response.";
RL Development 129:4739-4751(2002).
DR EMBL; AF483028; AAM76108.1; -.
```

```

QY 144 -BELPAAL-KACEAG-----RVTRYGIA----VLGHY 169
DB 62 AQVPEAIRKAVBAGKKRMKIKVPTVGTIPHEVMGHY 98

RESULT 7
PLAL_PLAAC STANDARD; PRT; 179 AA.
ID PLAL_PLAAC AC Q8GT41; P82817;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative invertase inhibitor precursor (Pollen allergen Pla a 1).
OS Platanus acerifolia (London plane tree).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Proteales; Platanaceae;
OC Platanus.
OX NCBI_TaxID=140101;
RN [1]
SEQUENCE FROM N.A., SEQUENCE OF 24-35; 49-55; 61-71; 113-121 AND
RP 151-158, AND TISSUE SPECIFICITY.
RP TISSUE=Pollen;
RX MEDLINE=22744443; PubMed=12859456;
RA Asturias J.A., Ibarrola I., Braso E., Arilla M.C., Martinez A.;
RT "The major Platanus acerifolia pollen allergen Pla a 1 has sequence
RT homology to invertase inhibitors.";
RL Clin. Exp. Allergy 33:978-985(2003).
CC -!- FUNCTION: Invertase inhibitor (Potential).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Pollen and stem, but not leaves.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC of the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (see http://www.isb-sib.ch/announcement
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ427413; CAD20556.1; -;
DR InterPro; IPR006501; PME_inhib.
DR InterPro; IPR007186; PME1.
DR Pfam; PF04043; PME1; 1.
DR TIGRFAMs; TIGR01614; PME_inhib; 1.
DR Allergen; Direct protein sequencing; Signal.
FT SIGNAL 1 23
FT CHAIN 24 179 Putative invertase inhibitor.
FT DISULFID 31 46 By similarity.
FT DISULFID 102 142 By similarity.
SQ SEQUENCE 179 AA; 19282 MW; 152B025B98879C5A CRC64;

Query Match 7.8%; Score 79.5; DB 1; Length 179;
Best local Similarity 24.8%; Pred. No. 51;
Matches 34; Conservative 25; Mismatches 39; Indels 39; Gaps 7

QY 13 QGSLAPTAQRCPTY-----MDVVIVLDGNSIYPWSEVQTFELRLIV 53
DB 28 QGTCKKVAQRSPNVNYDFCVKSLGADPKSHTDALQGLGVISANLAIQHGSKIQTIGRIL 87
QY 54 GKLFIDPEIQ-----VGLVQYGSPVHWSLGFRTKEEVVRAAKNISRRREGRTKTAQ 108
DB 88 -KSKVDPALKKYLNDVGLYADAKSSVQE-AIADFKSKD---YASANV-----KMSA 134
QY 109 AI--MWACTEGFSQSHG 123
DB 135 ALDDSVTCEDGFKKKG 151

RESULT 8
Q622B0 PRELIMINARY; PRT; 181 AA.
ID Q622B0
AC Q622B0;

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RA Rabbinoitsch E., Ruchner-Lord K., Tumapa S., Vesaratchavest M.,
 RA Songelivilai S., Stevens K., Barrell B.G., Oyaton P.C.F., Parkhill J.;
 RA Whitehead S., Yeates C., Barrell B.G., Oyaton P.C.F., Parkhill J.;
 RT "Genomic plasticity of the causative agent of melioidosis,
 Burkholderia pseudomallei";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
 DR ENBL; BX571966; CAH38548.1; --
 SQ SEQUENCE 184 AA; 20280 MW; 4C81CE777D6078B2 CRC64;

Query Match 7.1%; Score 72.5; DB 2; Length 184;
 Best Local Similarity 28.1%; Pred. No. 2.2e+02;
 Matches 38; Conservative 20; Mismatches 44; Indels 33; Gaps 10

QY 53 VGKLFDPQIQVGLVQYGESPVHEWSLG-----DF---RTKEEVVRAKNLSRREG--- 101
 DB 34 IGAL-MDDPAIPLRFL-----PWLAWHLGVETWKDYWPQVQRARVKAIRIARKKGTAA 87
 QY 102 --RETAKTAQAIMVACTEGFSQSHGGRPEARLLVVVTTDGHSDGELPAALK-----ACE 154
 DB 88 AVREVCASGANVAMREWEKTPKGRPGTFEILMTV---GARDG--IPATAEVADIAT 142
 QY 155 AGRTVRYGIAVLGHY 169
 DB 143 VDRAKR-GTA---HY 153

RESULT 13
 Q63YN4 PRELIMINARY; PRT; 184 AA.
 ID Q63YN4
 AC Q63YN4
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE Putative phage protein.
 GN ORFNames=BPSL0153;
 OS Burkholderia pseudomallei K96243.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=272560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K96243;
 RX PubMed=15377794;
 RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K., I.R.,
 RA Bentley S.D., Sebahia M., Thomson N.R., Bason N.R., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
 RA Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
 RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
 RA Rabbinoitsch E., Rutherford K., Sanders M., Simmonds M.,
 RA Songelivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
 RA Whitehead S., Yeates C., Barrell B.G., Oyaton P.C.F., Parkhill J.;
 RT "Genomic plasticity of the causative agent of melioidosis,
 Burkholderia pseudomallei";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245 (2004).
 DR ENBL; BX571965; CAH34140.1; --
 SQ SEQUENCE 184 AA; 20250 MW; 59C09A777D6078B2 CRC64;

Query Match 7.1%; Score 72.5; DB 2; Length 184;
 Best Local Similarity 28.1%; Pred. No. 2.2e+02;
 Matches 38; Conservative 20; Mismatches 44; Indels 33; Gaps 10

QY 53 VGKLFDPQIQVGLVQYGESPVHEWSLG-----DF---RTKEEVVRAKNLSRREG--- 101
 DB 34 IGAL-MDDPAIPLRFL-----PWLAWHLGVETWKDYWPQVQRARVKAIRIARKKGTAA 87
 QY 102 --RETAKTAQAIMVACTEGFSQSHGGRPEARLLVVVTTDGHSDGELPAALK-----ACE 154
 DB 88 AVREVCASGANVAMREWEKTPKGRPGTFEILMTV---GARDG--IPATAEVADIAT 142
 QY 155 AGRTVRYGIAVLGHY 169

```
Db 143 VDRKR-GTA---HY 153
RESULT 14
Q8KYU9 PRELIMINARY; PRT; 185 AA.
AC Q8KYU9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat shock protein HslV.
GN Name=hslV;
OS uncultured proteobacterium.
OC Bacteria; Proteobacteria; environmental samples.
OX NCBI_TaxID=153809;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21822632; PubMed=11832943; DOI=10.1038/415630a;
RA Beja O., Suzuki M.T., Heideberg J.F., Nelson W.C., Preston C.M.,
RA Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
RT "Unexpected diversity among marine aerobic anoxygenic phototrophs.";
RL Nature 415:630-633(2002).
DR EMBL; AE008921; AAM48724.1; -.
DR HSP; P43772; IOFH.
DR MEROPS; T01.006; -.
DR GO; GO:0005839; C:proteasome core complex (sensu Eukaryota); IEA.
DR GO; GO:0004175; F:endorpeptidase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR GO; GO:0006511; P:ubiquitin-dependent protein catabolism; IEA.
DR InterPro; IPR001353; Proteasome_A_B.
DR Pfam; PF00227; Proteasome; 1.
KW Heat shock.
SQ SEQUENCE 185 AA; 19430 MW; 9D882E3B14F28C6C CRC64;

Query Match 7.1%; Score 72.5; DB 2; Length 185;
Best Local Similarity 23.1%; Pred. No. 2.2e+02;
Matches 43; Conservative 20; Mismatches 68; Indels 55; Gaps 7;

Qy 13 QGSLAPTA-----QRCPTYMDVIVLDSNSIYPWSEVQTFLLRLVGLKLFIDPEQI 63
Db 30 QVSLGPTVIKGSARKVRLSPGNDVVVGFAGST-----ADAFLLERLEAKLEATPGQL 84
Qy 64 QVGLVQVGESPVHWSLGDPTKKEVVRAAKNLSRREGRETKTAQAIAIMVACTEGFSQSHG 123
Db 85 QRACVELAK---DW-----RTDKYLOKLEA-----MLIVTDG----- 113
Qy 124 GRPEAARLLVVVTGESHGDELPALKAACEAGRVTRYGIAVLGHYLRQRDPSSFLREI 183
Db 114 -----AELLIIITGAGDVLEPSHGIAAI-----GSGGNFALAAARGLQETDLNABEIAKA 163
Qy 184 RTIASD 189
Db 164 MAIASD 169

RESULT 15
Q6K2K8 PRELIMINARY; PRT; 187 AA.
AC Q6K2K8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein OSJNBa0091C16.20 (Hypothetical protein
DE P0519B12.40).
GN Name=OSJNBa0091C16.20; Synonyms=P0519B12.40;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
SEQUENCE FROM N.A.
```

```
RA Sasaki T., Matsumoto T., Katayose Y.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005820; BAD22464.1; -.
DR EMBL; AP004884; BAD21948.1; -.
KW Hypothetical protein.
SQ SEQUENCE 187 AA; 20415 MW; 96A0FCC9628681DE CRC64;

Query Match 7.1%; Score 72.5; DB 2; Length 187;
Best Local Similarity 26.0%; Pred. No. 2.3e+02;
Matches 53; Conservative 17; Mismatches 73; Indels 61; Gaps 11;

Qy 9 SFQPGSLAPTAQRCPTYMDVIVLDSNSI-----YPSSEVQTFLLRLVGLKLFIDPEQI 63
Db 16 SFSPPG-----PLTRDIYILSPNPLIPTPFSGYQSP-----RRLVA----- 52
Qy 64 QVGLVQVGESPVHWSLGDPTKKEVVRAAKNLSRREGRETKTAQAIAIMVACTEGFSQ--- 120
Db 53 -----VAARASGWRLWRLHGWRR-----TGAGGIARR-----TAQVTHDGVGDARRWR 98
Qy 121 -----SHG-GRPEAARLLVVVTGESHGDELPALKAACEAGRVTRYGIAVLG-----H 168
Db 99 HRTTAVVAHGVGRPDYPPSMPVPDGHAGHRLPD--RPCGHSGT--GTWVSGRAWNR 154
Qy 169 YLRQRDPSSFLREIRTIASDPDS 192
Db 155 STRAQPDPLPSLPSMEVAAAVPTD 178

Search completed: April 6, 2005, 14:40:36
Job time : 188 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 14:15:53 ; Search time 178 Seconds
(without alignments)
430.217 Million cell updates/sec

Title: US-09-647-544-2_COPY_140_337

Perfect score: 1025
Sequence: 1 GICARVDASFQPGSLAPTA.....FLREIRTIASDPDERFFENV 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760391 residues

Total number of hits satisfying chosen parameters: 1433677

Minimum DB seq length: 0
Maximum DB seq length: 198

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1:	Geneseqp1980s:*
2:	Geneseqp1990s:*
3:	Geneseqp2000s:*
4:	Geneseqp2001s:*
5:	Geneseqp2002s:*
6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	912	89.0	195	5 AAU76862	Aau76862 Human int
2	912	89.0	195	5 AAU76853	Aau76853 Human int
3	912	89.0	198	8 ADR23227	Adr23227 Human int
4	492	48.0	193	5 AAU76863	Aau76863 Human int
5	492	48.0	193	5 AAU76854	Aau76854 Human int
6	492	48.0	196	8 ADR23228	Adr23228 Human int
7	427	41.7	198	8 ADR23225	Adr23225 Human int
8	424	41.4	192	6 AAE33535	Aae33535 Rat-human
9	424	41.4	192	6 AAE33537	Aae33537 Human alp
10	419	40.9	192	6 AAE33536	Aae33536 Rat alpha
11	417	40.7	195	5 AAU76851	Aau76851 Human int
12	417	40.7	195	5 AAU76860	Aau76860 Human int
13	399	38.9	198	8 ADR23226	Adr23226 Human int
14	393	38.3	198	5 ABP54908	Abp54908 Integrin
15	389	38.0	195	5 AAU76852	Aau76852 Human int
16	389	38.0	195	5 AAU76861	Aau76861 Human int
17	374	36.5	185	4 AAU09125	Aau09125 Human int
18	285.5	27.9	148	4 AAU18634	Aau18634 Human nov
19	285.5	27.9	148	4 AAU19794	Aau19794 Human nov
20	285.5	27.9	148	5 ABP47854	Abp47854 Human pol
21	285.5	27.9	148	5 ABP48014	Abp48014 Human pol
22	285.5	27.9	148	7 ADC10816	Adc10816 Human ext
23	285.5	27.9	148	7 ADC10976	Adc10976 Human pro
24	282	27.5	103	4 AAU19822	Aau19822 Human nov
25	282	27.5	103	4 AAU87675	Aau87675 Novel cen

26	282	27.5	103	5 ABP48042	Abp48042 Human pol
27	282	27.5	103	7 ADC11004	Adc11004 Human pro
28	282	27.5	103	8 ADI54990	Adi54990 Novel hum
29	281	27.4	99	5 ADR41441	Adr41441 Human CD-
30	244	23.8	176	5 ABB78816	Abb78816 Von Wille
31	210.5	20.5	181	4 ABUS2684	Abu52684 Cell etru
32	179	17.5	180	5 ABP54907	Abp54907 Von Wille
33	177.5	17.3	195	8 ADR23229	Adr23229 Human int
34	171.5	16.7	192	5 AAU76864	Aau76864 Human int
35	171.5	16.7	192	5 AAU76855	Aau76855 Human int
36	156	15.2	194	8 ADR23223	Adr23223 Human int
37	151	14.7	194	8 ADR23222	Adr23222 Human int
38	149.5	14.6	186	8 ADM97129	Adm97129 Collagen
39	149	14.5	191	5 AAU76859	Aau76859 Human int
40	149	14.5	191	5 AAU76850	Aau76850 Human int
41	148	14.4	180	5 ABB76376	Abb76376 Lymphocyt
42	148	14.4	184	3 AAY82349	Aay82349 Human CD1
43	148	14.4	184	6 ABU07332	Abu07332 Human exp
44	148	14.4	184	8 ADG38995	Adg38995 Human CD1
45	148	14.4	184	8 ADR03370	Adr03370 Human CD1

ALIGNMENTS

RESULT 1

AAU76862
ID AAU76862 standard; protein; 195 AA.

XX AC AAU76862;

XX DT 21-MAY-2002 (first entry)

XX DE Human integrin alpha subunit Alpha 10 variant A domain.

XX KW Human; integrin alpha subunit; A domain; Alpha 10; integrin beta subunit;
A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
XX KW ischaemia-reperfusion injury; immune complex; parasitic disease; mutant;
XX KW antiinflammatory; vasotropic; antiparasitic; vulnery; gene therapy;
muteln.

XX OS Homo sapiens.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 193 /note= "Wild-type Ile substituted by any other amino acid"

XX FT

XX WO200209737-A1.

XX PD 07-FEB-2002.

XX PF 31-JUL-2001; 2001WO-US023957.

XX PR 31-JUL-2000; 2000US-0221950P.

XX PR 11-JAN-2001; 2001US-00758493.

XX PR 13-MAR-2001; 2001US-00805354.

XX PA (GENO) GEN HOSPITAL CORP.

XX PI Arnaout AM, Li R, Xiong J;

XX DR WPI; 2002-188687/24.

XX PT Novel high affinity integrin polypeptide useful for treating restenosis
and parasitic diseases, comprises all or part of variant integrin alpha
subunit A domain or variant integrin beta subunit A-like domain.

XX PS Claim 53; Page; 55pp; English.

XX CC The invention relates to a high affinity integrin polypeptide comprising
all or part of a variant integrin alpha subunit A domain or a variant

CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC integrin alpha subunit Alpha 10 variant A domain. Note: This variant
 CC sequence is not featured in the specification but has been derived from
 CC the wild-type protein shown in AAU76853

XX SQ Sequence 195 AA;

Query Match 89.0%; Score 912; DB 5; Length 195;
 Best Local Similarity 100.0%; Pred. No. 2e-96;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEIQVGLVQYGSPPVHWSLGD 82
 DB 1 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEIQVGLVQYGSPPVHWSLGD 60
 QY 83 FRTKEEVVRAAKNLSRREGRETAKQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 142
 DB 61 FRTKEEVVRAAKNLSRREGRETAKQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 120
 QY 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
 DB 121 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 2

AAU76853
 ID AAU76853 standard; protein; 195 AA.

AC AAU76853;

DT 21-MAY-2002 (first entry)

XX Human integrin alpha subunit Alpha 10 A domain.

XX Human; integrin alpha subunit; A domain; Alpha 10; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease;
 KW antiinflammatory; vasotropic; antiparasitic; vulnerability; gene therapy.

XX Homo sapiens.

XX WO200209737-A1.

XX 07-FEB-2002.

XX 31-JUL-2001; 2001WO-US023957.

XX 31-JUL-2000; 2000US-0221950P.

XX 11-JAN-2001; 2001US-00758493.

XX 13-MAR-2001; 2001US-00805354.

XX (GEO) GEN HOSPITAL CORP.

XX Arnaut AM, Li R, Xiong J;

XX WPI; 2002-188687/24.

XX Novel high affinity integrin polypeptide useful for treating restenosis

XX and parasitic diseases, comprises all or part of variant integrin alpha

XX subunit A domain or variant integrin beta subunit A-like domain.

XX Example 2; Fig 5; 55pp; English.

XX The invention relates to a high affinity integrin polypeptide comprising
 CC all or part of a variant integrin alpha subunit A domain or a variant
 CC integrin beta subunit A-like domain. The polypeptide, preferably the
 CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by
 CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 CC for determining if a test compound is a candidate compound for binding to
 CC CD11b or for treating an inflammatory disorder, by contacting a test
 CC compound with the polypeptide and determining if the test compound binds
 CC to the polypeptide. The integrin subunits are useful for reducing
 CC skeletal muscle injury, for treating disorders caused by ischaemia-
 CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 CC to purify variant integrin polypeptide ligands and as bait proteins in
 CC two-hybrid or three-hybrid assays. This sequence represents the human
 CC integrin alpha subunit Alpha 10 A domain

XX SQ Sequence 195 AA;

Query Match 89.0%; Score 912; DB 5; Length 195;
 Best Local Similarity 100.0%; Pred. No. 2e-96;
 Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEIQVGLVQYGSPPVHWSLGD 82
 DB 1 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEIQVGLVQYGSPPVHWSLGD 60
 QY 83 FRTKEEVVRAAKNLSRREGRETAKQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 142
 DB 61 FRTKEEVVRAAKNLSRREGRETAKQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 120
 QY 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
 DB 121 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 3

ADR23227
 ID ADR23227 standard; protein; 198 AA.

AC ADR23227;

XX 04-NOV-2004 (first entry)

XX Human integrin alpha 10 subunit A domain.

XX Human; integrin; inflammation; antiinflammatory; vasotropic.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Domain 1..195

XX /label = A_domain

XX Misc-difference 193

XX /note= "Invariant Ile residue"

XX WO2004066914-A2.

XX 12-AUG-2004.

XX 12-MAY-2003; 2003WO-US014919.

XX 10-MAY-2002; 2002US-00144259.

XX (GEO) GEN HOSPITAL CORP.

XX Arnaut MA, Li R, Xiong J;

XX WPI; 2004-593980/57.

XX GENBANK; XP_002097.

XX Novel variant integrin CD11b alpha subunit polypeptide, useful for
 XX determining candidate compound for binding to CD11b, and for determining


```
OS Homo sapiens.
XX WO200209737-A1.
XX 07-FEB-2002.
XX 31-JUL-2001; 2001WO-US023957.
XX 31-JUL-2000; 2000US-0221950P.
XX 11-JAN-2001; 2001US-00758493.
XX 13-MAR-2001; 2001US-00805354.
XX (GEO) GEN HOSPITAL CORP.
XX Arnaout AM, Li R, Xiong J;
XX WPI; 2002-188687/24.
XX Novel high affinity integrin polypeptide useful for treating restenosis
XX and parasitic diseases, comprises all or part of variant integrin alpha
XX subunit A domain or variant integrin beta subunit A-like domain.
XX Example 2; Fig 5; 55pp; English.
XX The invention relates to a high affinity integrin polypeptide comprising
XX all or part of a variant integrin alpha subunit A domain or a variant
XX integrin beta subunit A-like domain. The polypeptide, preferably the
XX CD11b alpha subunit A domain, where I at residue 332 has been replaced by
XX G or A, F at residue 313 and A at residue 320 have been replaced by C, or
XX V at residue 315 and A at residue 320 have been replaced by C, is useful
XX for determining if a test compound is a candidate compound for binding to
XX CD11b or for treating an inflammatory disorder, by contacting a test
XX compound with the polypeptide and determining if the test compound binds
XX to the polypeptide. The integrin subunits are useful for reducing
XX skeletal muscle injury, for treating disorders caused by ischaemia-
XX reperfusion injury, immune complexes, restenosis and parasitic diseases,
XX to purify variant integrin polypeptide ligands and as bait proteins in
XX two-hybrid or three-hybrid assays. This sequence represents the human
XX integrin alpha subunit Alpha 11 A domain
XX Sequence 193 AA;
XX Query Match 48.0%; Score 492; DB 5; Length 193;
XX Best Local Similarity 54.5%; Pred. No. 6.4e-48;
XX Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;
QY 23 CPTYMDVIVILDGNSIYPWSEVQTFLLRLVGLKFLDPDQIQLVQYGSPPHWSLGD 82
DB 1 CQTYMDIVILDGNSIYPWVEVQHFLNLTKKFIYIGPGQIQVGWQYGVGVHFEFLND 60
QY 83 FRTKEEVVRAAKNLSRRREGRETAKQAIMVACTGFSQSHGGRPEARLLVWVTDGSHD 142
DB 61 YRSVKDVVEAASHIEQGGTGTETATGIEPARSEAFQK--GGRKGAKVMIVITDGSHD 118
QY 143 GEELPAALKAACEAGRVTRYGIVGLHYLRQRDPSSFLREIRTIASDPDRFFPNV 198
DB 119 SPDLKVIQOSERDNTVRYAVAVLGYNRRNGINPETFLEIKVIASDPDDKHFNV 174
RESULT 6
ID ADR23228
XX ADR23228 standard; protein; 196 AA.
XX AC ADR23228;
XX AC ADR23228;
XX DT 04-NOV-2004 (first entry)
XX Human integrin alpha 11 subunit A domain.
XX Human; integrin; inflammation; antiinflammatory; vasotropic.
XX Homo sapiens.
XX
```

```
PH Key Location/Qualifiers
FT Domain 1..193
FT Misc-difference 191 /label = A_domain
FT /note= "Invariant Ile residue"
XX WO2004066914-A2.
XX 12-AUG-2004.
XX 12-MAY-2003; 2003WO-US014919.
XX 10-MAY-2002; 2002US-00144259.
XX (GEO) GEN HOSPITAL CORP.
XX Arnaout MA, Li R, Xiong J;
XX WPI; 2004-593980/57.
XX GENBANK; NP_036343.
XX Novel variant integrin CD11b alpha subunit polypeptide, useful for
XX determining candidate compound for binding to CD11b, and for determining
XX compound as activation-dependent ligand.
XX Disclosure; SEQ ID NO 8; 128pp; English.
XX The present sequence is that of the human integrin alpha 11 subunit A
XX domain. This includes an invariant Ile residue. The invention features a
XX variant integrin alpha subunit polypeptides in which the invariant Ile is
XX substituted by Gly, Ala or some other amino acid (e.g. Val) or is
XX deleted. The polypeptide can include part or all of the A domain.
XX Replacing the invariant Ile creates a variant integrin polypeptide that
XX is more active (i.e. in solution has a greater proportion of ligand-
XX forming polypeptides) than the wild-type form of the subunit. Variant
XX integrin polypeptides of the invention are useful in assays for compounds
XX that bind to a variant ligand, that interfere with or enhance the binding
XX of an integrin ligand to integrin, and for identifying activation-
XX specific ligands. They are also useful for generating antibodies, e.g.
XX monoclonal antibodies, which bind to the high efficiency form of an
XX integrin. Some such antibodies recognise an epitope that is either not
XX present or not accessible on an integrin that is in a lower affinity
XX conformation. The invention also provides methods of administering a
XX variant integrin polypeptide, or an antibody that selectively binds it,
XX to identify a ligand which binds to an active integrin. Such assays are
XX useful for diagnosing inflammation, e.g. occult inflammation (e.g.
XX abscess or an active arteriosclerotic lesion). Variant integrin
XX polypeptides can also be used to affect the bioavailability of a variant
XX integrin polypeptide ligand and to treat disorders associated with
XX aberrant or unwanted integrin expression or activity, such as vascular
XX injury.
XX Sequence 196 AA;
XX Query Match 48.0%; Score 492; DB 8; Length 196;
XX Best Local Similarity 54.5%; Pred. No. 6.5e-48;
XX Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;
QY 23 CPTYMDVIVILDGNSIYPWSEVQTFLLRLVGLKFLDPDQIQLVQYGSPPHWSLGD 82
DB 1 CQTYMDIVILDGNSIYPWVEVQHFLNLTKKFIYIGPGQIQVGWQYGVGVHFEFLND 60
QY 83 FRTKEEVVRAAKNLSRRREGRETAKQAIMVACTGFSQSHGGRPEARLLVWVTDGSHD 142
DB 61 YRSVKDVVEAASHIEQGGTGTETATGIEPARSEAFQK--GGRKGAKVMIVITDGSHD 118
QY 143 GEELPAALKAACEAGRVTRYGIVGLHYLRQRDPSSFLREIRTIASDPDRFFPNV 198
DB 119 SPDLKVIQOSERDNTVRYAVAVLGYNRRNGINPETFLEIKVIASDPDDKHFNV 174
RESULT 7
ADR23225
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```
ID ADR23225 standard; protein; 198 AA.
XX
AC ADR23225;
XX
DT 04-NOV-2004 (first entry)
XX
XX Human integrin CD49a alpha subunit A domain.
XX
XX Human; integrin; CD49a; inflammation; antiinflammatory; vasotropic.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 1..195
XX FT /label = A_domain
XX FT Misc-difference 193
XX FT /note= "Invariant Ile residue"
XX
XX PN W02004066914-A2.
XX
XX PD 12-AUG-2004.
XX
XX PF 12-MAY-2003; 2003WO-US014919.
XX
XX PR 10-MAY-2002; 2002US-00144259.
XX
XX PA (GEHO ) GEN HOSPITAL CORP.
XX
XX PI Arnaout MA, Li R, Xiong J;
XX
XX DR WPI; 2004-591980/57.
XX
XX DR GENBANK; P56199.
XX
XX PT Novel variant integrin CD11b alpha subunit polypeptide, useful for
XX determining candidate compound for binding to CD11b, and for determining
XX compound as activation-dependent ligand.
XX
XX PS Disclosure; SEQ ID NO 5; 128pp; English.
XX
XX The present sequence is that of the human integrin alpha subunit CD49a A
XX domain. This includes an invariant Ile residue. The invention features
XX variant integrin alpha subunit polypeptides in which the invariant Ile is
XX substituted by Gly, Ala or some other amino acid (e.g. Val) or is
XX deleted. The polypeptide can include part or all of the A domain.
XX Replacing the invariant Ile creates a variant integrin polypeptide that
XX is more active (i.e. in solution has a greater proportion of ligand-
XX forming polypeptides) than the wild-type form of the subunit. Variant
XX integrin polypeptides of the invention are useful in assays for compounds
XX that bind to a variant ligand, that interfere with or enhance the binding
XX of an integrin ligand to integrin, and for identifying activation-
XX specific ligands. They are also useful for generating antibodies, e.g.
XX monoclonal antibodies, which bind to the high efficiency form of an
XX integrin. Some such antibodies recognise an epitope that is either not
XX present or not accessible on an integrin that is in a lower affinity
XX conformation. The invention also provides methods of administering a
XX variant integrin polypeptide, or an antibody that selectively binds it,
XX to identify a ligand which binds to an active integrin. Such assays are
XX useful for diagnosing inflammation, e.g. occult inflammation (e.g.
XX abscess or an active arteriosclerotic lesion). Variant integrin
XX polypeptides can also be used to affect the bioavailability of a variant
XX integrin polypeptide ligand and to treat disorders associated with
XX aberrant or unwanted integrin expression or activity, such as vascular
XX injury.
XX
XX SQ Sequence 198 AA;
XX
XX Query Match 41.7%; Score 427; DB 8; Length 198;
XX Best Local Similarity 46.6%; Pred. NO. 2.1e-40;
XX Matches 82; Conservative 33; Mismatches 61; Indels 0; Gaps 0;
XX
XX 23 CPTVMVIVLDGNSNLYPWEVOTFLRLVGLKLFIDPEQIQVGLVQYGVSPVHWSLGD 82
XX | : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
XX 1 CSTOLDIVLDGNSNLYPWSVTAFLNDLLKRMIDGPKQVGLVQYGVNTHFNLUNK 60
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CC periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC rat-human alpha 1-I domain fusion protein, RdeltaH. This sequence is used
 CC in the exemplification of the invention. (Updated on 23-OCT-2003 to
 CC standardise OS field)
 XX Sequence 192 AA;
 SQ

Query Match 41.4%; Score 424; DB 6; Length 192;
 Best Local Similarity 47.1%; Pred. No. 4.5e-40;
 Matches 82; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

Qy 25 TYMDVIVLDGNSIYPWSEVQTFRLRLVGLKFLDPQIQVGLVQYQGESPVHWSLGDPR 84
 Db 1 TQLDIVIVLDGNSIYPWSEVQTFRLRLVGLKFLDPQIQVGLVQYQGESPVHWSLGDPR 84
 Qy 85 TKEEVVPAANKLSRREGRETQAQIMVACTEGFSQSHGGRPEARLLVVVTGDSHGE 144
 Db 61 STEEVLVAANKIVQGRGRTMTALGIDTARKEAFTEARGARRGVKKVMVIVTGESHDNY 120
 Qy 145 ELPAALKACBAGRVTRYGIAVLGHYLRQRDPSPFLREIRTIASDPDERFFNV 198
 Db 121 RLKXVIQDCEDENIQRFSAIILGNYNGNLSTKFEVEIKSIASEPTEKHFFNV 174

RESULT 9
 AAEE33537
 ID AAEE33537 standard; protein; 192 AA.
 AC AAEE33537;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Human alpha 1-I domain protein #1.
 XX
 KW Human; very late activation antigen; VLA-1; betal containing integrin;
 KW immunological disorder; inflammatory disorder; skin related condition;
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa;
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KW graft versus host disease; myocardial ischaemia; alpha 1-I protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200283854-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 12-APR-2002; 2002WO-US011521.
 XX
 PR 13-APR-2001; 2001US-0283794P.
 PR 06-JUL-2001; 2001US-0303689P.
 XX
 XX (BIOJ) BIOGEN INC.
 PA
 XX Lyne PD, Garber EA, Saldanha JW, Karpusas M;
 PI
 XX WPI; 2003-093009/08.
 DR
 XX New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-

PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
 PT fibrosis.
 XX
 PS Example 24; Page 94; 248pp; English.
 XX
 CC The present invention relates to novel antibodies that specifically bind
 CC to very late activation (VLA-1; betal containing integrins) antigens and
 CC methods of using these antibodies to treat immunological disorders. The
 CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 CC mediated immunological or inflammatory disorders such as skin related
 CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 CC periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 CC autoimmune diseases (e.g. type I diabetes, myasthenia gravis, rheumatoid
 CC arthritis, systemic lupus erythematosus and multiple sclerosis), renal
 CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 CC immediate hypersensitivity), graft and transplant rejections, graft
 CC versus host disease, conjunctivitis, swelling occurring after injury,
 CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 CC human 1-I domain protein. This sequence is used in the exemplification of
 CC the invention
 XX
 SQ Sequence 192 AA;
 Query Match 41.4%; Score 424; DB 6; Length 192;
 Best Local Similarity 47.1%; Pred. No. 4.5e-40;
 Matches 82; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

Qy 25 TYMDVIVLDGNSIYPWSEVQTFRLRLVGLKFLDPQIQVGLVQYQGESPVHWSLGDPR 84
 Db 1 TQLDIVIVLDGNSIYPWSEVQTFRLRLVGLKFLDPQIQVGLVQYQGESPVHWSLGDPR 84
 Qy 85 TKEEVVPAANKLSRREGRETQAQIMVACTEGFSQSHGGRPEARLLVVVTGDSHGE 144
 Db 61 STEEVLVAANKIVQGRGRTMTALGIDTARKEAFTEARGARRGVKKVMVIVTGESHDNY 120
 Qy 145 ELPAALKACBAGRVTRYGIAVLGHYLRQRDPSPFLREIRTIASDPDERFFNV 198
 Db 121 RLKXVIQDCEDENIQRFSAIILGNYNGNLSTKFEVEIKSIASEPTEKHFFNV 174

RESULT 10
 AAEE33536
 ID AAEE33536 standard; protein; 192 AA.
 AC AAEE33536;
 XX
 DT 02-APR-2003 (first entry)
 XX
 DE Rat alpha 1-I domain protein #1.
 XX
 KW Rat; very late activation antigen; VLA-1; betal containing integrin;
 KW immunological disorder; inflammatory disorder; skin related condition;
 KW psoriasis; eczema; burn; dermatitis; respiratory distress syndrome;
 KW fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bursitis;
 KW fever; migraine headache; inflammatory bowel disease; Crohn's disease;
 KW irritable bowel syndrome; colitis; colorectal cancer; vascular disease;
 KW atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa;
 KW gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease;
 KW osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis;
 KW systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome;
 KW renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis;
 KW hypersensitivity; graft rejection; transplant rejection; conjunctivitis;
 KW graft versus host disease; myocardial ischaemia; alpha 1-I protein.
 XX
 OS Rattus sp.

XX PN WO200283854-A2.
 XX PD 24-OCT-2002.
 XX PF 12-APR-2002; 2002WO-US011521.
 XX PR 13-APR-2001; 2001US-0283794P.
 XX PR 06-JUL-2001; 2001US-0303689P.
 XX PA (BIOJ) BIOGEN INC.
 XX PI Lyne PD, Garber EA, Saldanha JW, Karpueas M;
 XX PF WPI; 2003-093009/08.
 XX DR
 XX PT New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 XX PT mediated immunological or inflammatory disorders, e.g. psoriasis, eczema,
 XX PT burns, dermatitis, and abnormal proliferation of hair follicle cells or
 XX PT fibrosis.
 XX PS
 XX PS Example 24; Page 93-94; 248pp; English.
 XX CC The present invention relates to novel antibodies that specifically bind
 XX CC to very late activation (VLA-1; beta1 containing integrins) antigens and
 XX CC methods of using these antibodies to treat immunological disorders. The
 XX CC anti-VLA-1 antibodies are useful for preventing or treating VLA-1-
 XX CC mediated immunological or inflammatory disorders such as skin related
 XX CC conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal
 XX CC proliferation of hair follicle cells), fibrosis (e.g. kidney or lung
 XX CC fibrosis), allergic rhinitis, respiratory distress syndrome, asthma,
 XX CC bronchitis, tendonitis, bursitis, fever, migraine headaches, gastro-
 XX CC intestinal conditions (e.g. inflammatory bowel disease, Crohn's disease,
 XX CC gastritis, irritable bowel syndrome, colitis and colorectal cancer),
 XX CC vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia,
 XX CC parietaritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis,
 XX CC autoimmune diseases (e.g. type I diabetes, rheumatoid arthritis, multiple
 XX CC sclerosis, systemic lupus erythematosus and multiple sclerosis), renal
 XX CC failure, sarcoidosis, nephrotic syndrome, Behcet's syndrome, gingivitis,
 XX CC polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or
 XX CC immediate hypersensitivity), graft and transplant rejections, graft
 XX CC versus host disease, conjunctivitis, swelling occurring after injury,
 XX CC myocardial ischaemia or endotoxin shock syndrome. The present sequence is
 XX CC rat 1-I domain protein. This sequence is used in the exemplification of
 XX CC the invention
 XX SQ Sequence 192 AA;

Query Match 40.9%; Score 419; DB 6; Length 192;
 Best Local Similarity 46.6%; Pred. No. 1.7e-39;
 Matches 81; Conservative 33; Mismatches 60; Indels 0; Gaps 0;
 QY 25 TYMDVIVLDGNSIYPWSEVOTFLRLVGLKFLDPQIQVGLVOYGSPVHWSLGD 84
 Db 1 TQLDIVLDGNSIYPWSEVIAFLNDLLKMDLGPQTQVIGVQYGENVTHEFNLYS 60
 QY 85 TKEEVVRAAKNLSRREGRETAKQAQIMVACTEGFSQSHGGRPEAARLLVVVTDGSHDGE 144
 Db 61 STEEVLVAANKIGRQGGLOMTALGIDTARKEAFTARGARGVKVVMVITDGHSDNY 120
 QY 145 ELPAALKACAGRVTRYGVIAVLGHYLRQRDPSSFLREIRTIADPDERFFNV 198
 Db 121 RLKQVQDCEDENQRFSAIILGHYNRGNLSTEFKFEVEIKSIASEPTKHFNV 174

RESULT 11
 AAU76851
 ID AAU76851 standard; protein; 195 AA.
 XX AC AAU76851;
 XX AC
 XX DT 21-MAY-2002 (first entry)
 XX DT

DE XX Human integrin alpha subunit Alpha 1 (CD49a) A domain.
 XX KW Human; integrin alpha subunit; A domain; CD49a; integrin beta subunit;
 KW A-like domain; inflammatory disorder; skeletal muscle injury; restenosis;
 KW ischaemia-reperfusion injury; immune complex; parasitic disease; Alpha 1;
 KW antiinflammatory; vasotropic; antiparasitic; vulnerary; gene therapy.
 XX OS Homo sapiens.
 XX PN WO200209737-A1.
 XX PD 07-FEB-2002.
 XX PF 31-JUL-2001; 2001WO-US023957.
 XX PR 31-JUL-2000; 2000US-0221950P.
 XX PR 11-JAN-2001; 2001US-00758493.
 XX PR 13-MAR-2001; 2001US-00805354.
 XX PA (GEHO) GEN HOSPITAL CORP.
 XX PI Arnaout AM, Li R, Xiong J;
 XX PF WPI; 2002-188687/24.
 XX DR
 XX PT Novel high affinity integrin polypeptide useful for treating restenosis
 XX PT and parasitic diseases, comprises all or part of variant integrin alpha
 XX PT subunit A domain or variant integrin beta subunit A-like domain.
 XX PS
 XX PS Example 2; Fig 5; 55pp; English.
 XX CC The invention relates to a high affinity integrin polypeptide comprising
 XX CC all or part of a variant integrin alpha subunit A domain or a variant
 XX CC integrin beta subunit A-like domain. The polypeptide, preferably the
 XX CC CD11b alpha subunit A domain, where I at residue 332 has been replaced by C, or
 XX CC G or A, F at residue 313 and A at residue 320 have been replaced by C, or
 XX CC V at residue 315 and A at residue 320 have been replaced by C, is useful
 XX CC for determining if a test compound is a candidate compound for binding to
 XX CC CD11b or for treating an inflammatory disorder, by contacting a test
 XX CC compound with the polypeptide and determining if the test compound binds
 XX CC to the polypeptide. The integrin subunits are useful for reducing
 XX CC skeletal muscle injury, for treating disorders caused by ischaemia-
 XX CC reperfusion injury, immune complexes, restenosis and parasitic diseases,
 XX CC to purify variant integrin polypeptide ligands and as bait proteins in
 XX CC two-hybrid or three-hybrid assays. This sequence represents the human
 XX CC integrin alpha subunit Alpha 1 (CD49a) A domain
 XX SQ Sequence 195 AA;

Query Match 40.7%; Score 417; DB 5; Length 195;
 Best Local Similarity 45.5%; Pred. No. 3e-39;
 Matches 80; Conservative 34; Mismatches 62; Indels 0; Gaps 0;
 QY 23 CPTYMDVIVLDGNSIYPWSEVOTFLRLVGLKFLDPQIQVGLVOYGSPVHWSLGD 82
 Db 1 CSTQLDIVLDGNSIYPWDSVTAFLNDLLKMDIGKQIQVIGVQYGENVTHEFNLYS 60
 QY 83 FRTKEEVVRAAKNLSRREGRETAKQAQIMVACTEGFSQSHGGRPEAARLLVVVTDGSHD 142
 Db 61 YSSTEELVAANKIVQGRGQMTALGTDRTARKEAFTARGARGVKVVMVITDGHSD 120
 QY 143 GEELPAALKACAGRVTRYGVIAVLGHYLRQRDPSSFLREIRTIADPDERFFNV 198
 Db 121 NHRLKKVQDCEDENLQRFSAIILGHYNRGNLSTEFKFEVEIKSIASEPTKHFNV 176

RESULT 12
 AAU76860
 ID AAU76860 standard; protein; 195 AA.
 XX AC AAU76860;
 XX AC
 XX DT 21-MAY-2002 (first entry)
 XX DT

Matches 81; Conservative 29; Mismatches 66; Indels 0; Gaps 0;

Qy 23 CPTVMVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEQIQVGLVQVGSPPVHWSLGD 82
 Db 1 CPSLIDVVVVCDESNIYPWDVAVNFLEKFKVQGLDGTGPTKQVGLIQVANNPRVVFNLNT 60

Qy 83 FRTKEEVVRAAKNLSRREGRTKTAQAQIMVACTEGFSQSHGGRPEARLLVVTGDSHD 142
 Db 61 YKTEEMIVATSQTSQYGGDLTNTFGAIQYARKYAYSASGGRSAAATKVMVWVVDGESH 120

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
 Db 121 GSKLKAVIDQCNHNDILRFGIAVLGLYLRNALDTKNLIKELKAIASIPTEYFFNV 176

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
 Db 121 GSKLKAVIDQCNHNDILRFGIAVLGLYLRNALDTKNLIKELKAIASIPTEYFFNV 176

RESULT 14
 ID ABP54908 standard; protein; 198 AA.
 AC ABP54908;
 XX 08-JAN-2003 (first entry)
 DT Integrin alpha-2 I domain.
 DE Anthrax; toxin; receptor; integrin; human; antibacterial.
 KW Homo sapiens.
 OS WO200246228-A2.
 FN 13-JUN-2002.
 PD 03-OCT-2001; 2001WO-US030941.
 PF 05-DEC-2000; 2000US-0251481P.
 PR (WISC) WISCONSIN ALUMNI RES FOUND.
 PA Young JAT, Bradley KA, Collier RJ, Mogridge JS;
 PI WPI; 2002-713235/77.
 XX Novel isolated polypeptide useful for identifying agent that prevents or reduces effect of anthrax toxin on host cell, for treating human or non-human animal suffering from anthrax.
 PT Disclosure; Page 31-32; 45pp; English.

The present sequence is the I domain of human integrin alpha-2. Ligand binding through I domains requires an intact metal ion-dependent adhesion site (MIDAS) motif. A MIDAS motif has been identified in the extracellular domain of a newly identified human anthrax toxin receptor (ATR). The invention provides ATR polypeptides (see ABP54903-06) and polynucleotides (see ABP73981), vectors, host cells, and transgenic and knock-out animals. It also provides methods for identifying molecules that bind the ATR and which reduce the toxicity of anthrax toxin. A claimed method for treating anthrax in a human or animal involves administering an agent that inhibits binding between PA and ATR at a level effective to reduce the severity of anthrax. Suitable agents include ATR or a PA-binding fragment of ATR, a PA-binding polypeptide at least 80% identical to these, a fusion protein, a monoclonal or polyclonal antibody, a polysaccharide, a lipid or a nucleic acid

Sequence 198 AA;
 Query Match 38.3%; Score 393; DB 5; Length 198;
 Best Local Similarity 46.0%; Pred. No. 1.8e-36;
 Matches 81; Conservative 28; Mismatches 67; Indels 0; Gaps 0;

Qy 23 CPTVMVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEQIQVGLVQVGSPPVHWSLGD 82
 Db 1 CPSLIDVVVVCDESNIYPWDVAVNFLEKFKVQGLDGTGPTKQVGLIQVANNPRVVFNLNT 60

Qy 83 FRTKEEVVRAAKNLSRREGRTKTAQAQIMVACTEGFSQSHGGRPEARLLVVTGDSHD 142
 Db 61 YKTEEMIVATSQTSQYGGDLTNTFGAIQYARKYAYSASGGRSAAATKVMVWVVDGESH 120

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
 Db 121 GSKLKAVIDQCNHNDILRFGIAVLGLYLRNALDTKNLIKELKAIASIPTEYFFNV 176

RESULT 15
 ID AAU76852 standard; protein; 195 AA.
 AC AAU76852;
 XX 21-MAY-2002 (first entry)
 DT Human integrin alpha subunit Alpha 2 (CD49b) A domain.
 DE Human; integrin alpha subunit; A domain; CD49b; integrin beta subunit; A-like domain; inflammatory disorder; skeletal muscle injury; restenosis; ischaemia-reperfusion injury; immune complex; parasitic disease; Alpha 2; antiinflammatory; vasotropic; antiparasitic; pulmonary; gene therapy.
 KW Homo sapiens.
 OS WO200209737-A1;
 FN 07-FEB-2002.
 PD 31-JUL-2001; 2001WO-US023957.
 PF 31-JUL-2000; 2000US-0221950P.
 PR 11-JAN-2001; 2001US-00758493.
 PR 13-MAR-2001; 2001US-00805354.
 XX (GEHO) GEN HOSPITAL CORP.
 PA Arnaout AM, Li R, Xiong J;
 PI WPI; 2002-198687/24.
 XX Novel high affinity integrin polypeptide useful for treating restenosis and parasitic diseases, comprises all or part of variant integrin alpha subunit A domain or variant integrin beta subunit A-like domain.
 PT Example 2; Fig 5; 55pp; English.

The invention relates to a high affinity integrin polypeptide comprising all or part of a variant integrin alpha subunit A domain or a variant integrin beta subunit A-like domain. The polypeptide, preferably the CD11b alpha subunit A domain, where I at residue 332 has been replaced by G or A, F at residue 313 and A at residue 320 have been replaced by C, or V at residue 315 and A at residue 320 have been replaced by C, is useful for determining if a test compound is a candidate compound for binding to CD11b or for treating an inflammatory disorder, by contacting a test compound with the polypeptide and determining if the test compound binds to the polypeptide. The integrin subunits are useful for reducing skeletal muscle injury, for treating disorders caused by ischaemia-reperfusion injury, immune complexes, restenosis and parasitic diseases, to purify variant integrin polypeptide ligands and as bait proteins in two-hybrid or three-hybrid assays. This sequence represents the human integrin alpha subunit Alpha 2 (CD49b) A domain

Sequence 195 AA;
 Query Match 38.0%; Score 389; DB 5; Length 195;
 Best Local Similarity 44.9%; Pred. No. 5.1e-36;
 Matches 79; Conservative 30; Mismatches 67; Indels 0; Gaps 0;

Qy 23 CPTVMVIVLDGNSIYPWSEVQTFLLRLVGKLFIDPEQIQVGLVQVGSPPVHWSLGD 82
 Db 1 CPSLIDVVVVCDESNIYPWDVAVNFLEKFKVQGLDGTGPTKQVGLIQVANNPRVVFNLNT 60

```
Db      1 CPSLIDVVVVCDESNSIYPWDVAVKNFLEKFVQGLDIGFTKTQVGLIQYANNPRVVFNLNT 60
Qy      83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTEGFSQSHGGRPEAAARLLVVVTDGESH 142
Db      61 YKTKEEMIVATSQTSQYGGDLTNIFGAIQYARKYAYSAASGGRSATAKVMVVVTDGKSHD 120
Qy      143 GEELPAALKACEAGRVTTRYGIAVLGHYLRQRDPSPFLREIRTIASDPDERFFPNV 198
Db      121 GSKLKAVIDQCNDHNDILRFGIAVLGYLNRNALDTKNLIKAIASIPTERYPFNV 176
```

Search completed: April 6, 2005, 14:36:34
Job time : 180 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 14:37:40 ; Search time 138 Seconds
(without alignments)
476.344 Million cell updates/sec

Title: US-09-647-544-2_COPY_140_337
Perfect score: 1025
Sequence: 1 GICARVDASFPQGS LAPTA.....FLRIRTIASDPDRFFENV 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 839692

Minimum DB seq length: 0

Maximum DB seq length: 198

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	912	89.0	195	10	US-09-805-354-7
2	912	89.0	195	11	US-09-758-493-7
3	912	89.0	195	14	US-10-144-259-7
4	492	48.0	193	10	US-09-805-354-8
5	492	48.0	193	11	US-09-758-493-8
6	492	48.0	193	14	US-10-144-259-8
7	427	41.7	195	10	US-09-805-354-5
8	427	41.7	195	11	US-09-758-493-5
9	427	41.7	195	14	US-10-144-259-5
10	424	41.4	192	15	US-10-474-832-59
11	424	41.4	192	15	US-10-474-832-61
12	419	40.9	192	15	US-10-346-863-57
13	419	40.9	192	15	US-10-474-832-60
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 8, Appli
					Sequence 5, Appli
					Sequence 8, Appli
					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 5, Appli
					Sequence 59, Appli
					Sequence 61, Appli
					Sequence 57, Appli
					Sequence 60, Appli

14	399	38.9	195	10	US-09-805-354-6	Sequence 6, Appli
15	399	38.9	195	11	US-09-758-493-6	Sequence 6, Appli
16	399	38.9	195	14	US-10-144-259-6	Sequence 6, Appli
17	285.5	27.9	148	9	US-09-764-870-284	Sequence 284, App
18	285.5	27.9	148	9	US-09-764-870-444	Sequence 444, App
19	285.5	27.9	148	14	US-10-125-540-284	Sequence 284, App
20	285.5	27.9	148	14	US-10-125-540-444	Sequence 444, App
21	282	27.5	103	9	US-09-764-870-472	Sequence 472, App
22	282	27.5	103	11	US-09-764-875-1193	Sequence 1193, App
23	282	27.5	103	14	US-10-125-540-472	Sequence 472, App
24	244	23.8	176	10	US-09-976-782-38	Sequence 38, Appli
25	191	18.6	176	15	US-10-004-378A-79	Sequence 79, Appli
26	179	17.5	178	15	US-10-346-863-43	Sequence 43, Appli
27	179	17.5	180	15	US-10-346-863-31	Sequence 31, Appli
28	177.5	17.3	192	10	US-09-805-354-9	Sequence 9, Appli
29	177.5	17.3	192	11	US-09-758-493-9	Sequence 9, Appli
30	177.5	17.3	192	14	US-10-144-259-9	Sequence 9, Appli
31	175	17.1	150	15	US-10-346-863-30	Sequence 30, Appli
32	175	17.1	180	15	US-10-080-334-130	Sequence 130, App
33	172.5	16.8	180	15	US-10-346-863-40	Sequence 40, Appli
34	163	15.9	176	15	US-10-004-378A-81	Sequence 81, Appli
35	156	15.2	191	10	US-09-805-354-3	Sequence 3, Appli
36	156	15.2	191	11	US-09-758-493-3	Sequence 3, Appli
37	156	15.2	191	14	US-10-144-259-3	Sequence 3, Appli
38	150	14.6	166	15	US-10-074-978A-265	Sequence 265, App
39	148	14.4	182	15	US-10-346-863-33	Sequence 33, Appli
40	148	14.4	182	15	US-10-346-863-35	Sequence 35, Appli
41	148	14.4	183	15	US-10-346-863-36	Sequence 36, Appli
42	148	14.4	183	15	US-10-346-863-20	Sequence 20, Appli
43	148	14.4	183	15	US-10-346-863-41	Sequence 41, Appli
44	148	14.4	183	16	US-10-615-515-7	Sequence 7, Appli
45	148	14.4	184	10	US-09-805-354-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-805-354-7
; Sequence 7, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xi,ong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-805-354-7

Query Match 89.0%; Score 912; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	23	CPTVMDVVIVLDGNSIYPWSEVQTFRLRLVGKLFIDPEQIQVGLVOYGESPVHWSIGD	82
Db	1	CPTVMDVVIVLDGNSIYPWSEVQTFRLRLVGKLFIDPEQIQVGLVOYGESPVHWSIGD	60
Qy	83	FRTEEVVRAAKNLSRREGRETKTQAQIMVACTEGFSQSHGGRPEARLLVVVTDGESH	142
Db	61	FRTEEVVRAAKNLSRREGRETKTQAQIMVACTEGFSQSHGGRPEARLLVVVTDGESH	120

```
Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
Db 121 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 2
US-09-758-493-7
; Sequence 7, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-7

Query Match 89.0%; Score 912; DB 11; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CPTTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKFLIDPEQIQVGLVQYGSPPVHWSLGD 82
Db 1 CPTTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKFLIDPEQIQVGLVQYGSPPVHWSLGD 60

Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 142
Db 61 FRTKEEVVRAAKNLSRREGRETAKTAQIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 120

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
Db 121 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 3
US-10-144-259-7
; Sequence 7, Application US/10144259
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-7

Query Match 89.0%; Score 912; DB 14; Length 195;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 23 CPTTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKFLIDPEQIQVGLVQYGSPPVHWSLGD 82
Db 1 CPTTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKFLIDPEQIQVGLVQYGSPPVHWSLGD 60

Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 142
Db 61 FRTKEEVVRAAKNLSRREGRETAKTAQIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 120

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
Db 121 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 176

RESULT 4
US-09-805-354-8
; Sequence 8, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
; CURRENT FILING DATE: 2002-06-04
; PRIOR FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-8

Query Match 48.0%; Score 492; DB 10; Length 193;
Best Local Similarity 54.5%; Pred. No. 2.5e-44;
Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;

Qy 23 CPTTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKFLIDPEQIQVGLVQYGSPPVHWSLGD 82
Db 1 CPTTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKFLIDPEQIQVGLVQYGSPPVHWSLGD 60

Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQIMVACTEGFSQSHGGRPEAARLLVVVTDGESH 142
Db 61 YRSVKDVVEAAASHIEQRGGTETRTAFGIEFARSEAFQK--GGRKGAKKVMIVITDGESH 118

Qy 143 GEELPAALKACEAGRVTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
Db 119 SPDLKVIQSERDNTVRYAVAVLGYNRRGINPETFLNEIKYIASDPDDKHFFNV 174

RESULT 5
US-09-758-493-8
; Sequence 8, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 193
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-8

Query Match      48.0%; Score 492; DB 11; Length 193;
Best Local Similarity 54.5%; Pred. No. 2.5e-44;
Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;

Qy 23 CPTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CQTYMDIVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTGFSQSHGGRPEAAARLLVVVTDGSHD 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YRSVKDVVEAAASHLEQGGTETRTAFGLEFARSAFQK--GGRGAKKVMIVITDGSND 118
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 GEELPAALKACEAGRVTTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 SPDLEKVIQOSERDNTVYAVAVLGYNNRGINPETFLNEIKYIASDPDDKHFFNV 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 6
US-10-144-259-8
; Sequence 8, Application US/10144259
; Publication No. US20030105691A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-8

Query Match      48.0%; Score 492; DB 14; Length 193;
Best Local Similarity 54.5%; Pred. No. 2.5e-44;
Matches 96; Conservative 31; Mismatches 47; Indels 2; Gaps 1;

Qy 23 CPTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CQTYMDIVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTGFSQSHGGRPEAAARLLVVVTDGSHD 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YRSVKDVVEAAASHLEQGGTETRTAFGLEFARSAFQK--GGRGAKKVMIVITDGSND 118
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 GEELPAALKACEAGRVTTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 SPDLEKVIQOSERDNTVYAVAVLGYNNRGINPETFLNEIKYIASDPDDKHFFNV 174
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 7
US-09-805-354-5
; Sequence 5, Application US/09805354
; Publication No. US20030078375A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-536001
; CURRENT APPLICATION NUMBER: US/09/805,354
```

```
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-805-354-5

Query Match      41.7%; Score 427; DB 10; Length 195;
Best Local Similarity 46.6%; Pred. No. 2.4e-37;
Matches 82; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

Qy 23 CPTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CSTQLDIVIVLDGNSIYPWDSVTAFLNDLLKRMIDIGPKQTQVGIQYGENVTHEFNLNK 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTGFSQSHGGRPEAAARLLVVVTDGSHD 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YSSTEELVAAKKIVQGGRTWTALGTDARKEAFTARGARRGVKKVMIVITDGSND 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 GEELPAALKACEAGRVTTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 NHRLKKVIQDCEDENIQRFSAIILGNSYRNLSTKFEVFEIKSIASEPTEKHFFNV 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-758-493-5
; Sequence 5, Application US/09758493
; Publication No. US20040086935A1
; GENERAL INFORMATION:
; APPLICANT: Arnaout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: HIGH AFFINITY INTEGRIN POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 00786-804001
; CURRENT APPLICATION NUMBER: US/09/758,493
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-493-5

Query Match      41.7%; Score 427; DB 11; Length 195;
Best Local Similarity 46.6%; Pred. No. 2.4e-37;
Matches 82; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

Qy 23 CPTMDVVIVLDGNSIYPWSEVQTFLLRLVGLKLFIDPEIQVGLVQYGESPVHWSLGD 82
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 CSTQLDIVIVLDGNSIYPWDSVTAFLNDLLKRMIDIGPKQTQVGIQYGENVTHEFNLNK 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 83 FRTKEEVVRAAKNLSRREGRETAKTAQAIMVACTGFSQSHGGRPEAAARLLVVVTDGSHD 142
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 YSSTEELVAAKKIVQGGRTWTALGTDARKEAFTARGARRGVKKVMIVITDGSND 120
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 143 GEELPAALKACEAGRVTTRYGIAVLGHYLRQRDPSSFLREIRTIASDPDERFFNV 198
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 NHRLKKVIQDCEDENIQRFSAIILGNSYRNLSTKFEVFEIKSIASEPTEKHFFNV 176
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-10-144-259-5
; Sequence 5, Application US/10144259
```

```
; Publication No. US20030109691A1
; GENERAL INFORMATION:
; APPLICANT: Arnsout, M. Amin
; APPLICANT: Li, Rui
; APPLICANT: Xiong, Jian-Ping
; TITLE OF INVENTION: VARIANT INTEGRIN POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 00786-548001
; CURRENT APPLICATION NUMBER: US/10/144,259
; PRIOR FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/758,493
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: US 60/221,950
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-259-5

Query Match 41.4%; Score 427; DB 14; Length 195;
Best Local Similarity 46.6%; Pred. No. 2.4e-37;
Matches 82; Conservative 33; Mismatches 61; Indels 0; Gaps 0;

Qy 23 CPTVMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLIDPEIQVGLVQVGPVHWSLGD 82
Db 1 CSTQLDIVLDGNSIYPWDSVTAFLNDLLKRWIDIGPKQTQVGIQVGENVTHEFNLNK 60

Qy 83 PRKEVVRRAAKNLSRREGRETAKTAQAIMVACTEGFSQSHGGRPEAAARLLVVVTDGSHD 142
Db 61 YSSEELVVAAKIVQRRGRTMTALGDTARKEAFTARGARRGVKKVMVIVTDGSHD 120

Qy 143 GEEIPAAKACEAGRVTRYGIAVLGHYLRQRDSSFLREIRTASDPDERFFNV 198
Db 121 NHRLLKVIQDCDENIQRFSAIILGNSYNGNLSTKFEVEIKSIASEPTEKHFFNV 176

RESULT 10
US-10-474-832-59
; Sequence 59, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rat/human chimeric
; OTHER INFORMATION: I domain construct
US-10-474-832-59

Query Match 41.4%; Score 424; DB 15; Length 192;
Best Local Similarity 47.1%; Pred. No. 5e-37;
Matches 82; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

Qy 25 TYMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLIDPEIQVGLVQVGPVHWSLGD 84
Db 1 TQLDIVLDGNSIYPWDSVTAFLNDLLKRWIDIGPKQTQVGIQVGENVTHEFNLNK 60

Qy 85 TKEEVRRAAKNLSRREGRETAKTAQAIMVACTEGFSQSHGGRPEAAARLLVVVTDGSHD 144
Db 61 STEEVLVAAKIVQRRGRTMTALGDTARKEAFTARGARRGVKKVMVIVTDGSHD 120

RESULT 11
US-10-474-832-61
; Sequence 61, Application US/10474832
; Publication No. US20040081651A1
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: ANTIBODIES TO VLA-1
; CURRENT APPLICATION NUMBER: US/10/474,832
; CURRENT FILING DATE: 2003-10-14
; PRIOR APPLICATION NUMBER: 60/283,794
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/303,689
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-474-832-61

Query Match 41.4%; Score 424; DB 15; Length 192;
Best Local Similarity 47.1%; Pred. No. 5e-37;
Matches 82; Conservative 33; Mismatches 59; Indels 0; Gaps 0;

Qy 25 TYMDVIVLDGNSIYPWSEVQTFLLRLVGLKFLIDPEIQVGLVQVGPVHWSLGD 84
Db 1 TQLDIVLDGNSIYPWDSVTAFLNDLLKRWIDIGPKQTQVGIQVGENVTHEFNLNK 60

Qy 85 TKEEVRRAAKNLSRREGRETAKTAQAIMVACTEGFSQSHGGRPEAAARLLVVVTDGSHD 144
Db 61 STEEVLVAAKIVQRRGRTMTALGDTARKEAFTARGARRGVKKVMVIVTDGSHD 120

RESULT 12
US-10-346-863-57
; Sequence 57, Application US/10346863
; Publication No. US20040038325A1
; GENERAL INFORMATION:
; APPLICANT: PHELPS, CHRISTOPHER BENJAMIN
; APPLICANT: FAGAN, RICHARD JOSEPH
; APPLICANT: GUTTERIDGE, ALEX
; TITLE OF INVENTION: ADHESION MOLECULES
; FILE REFERENCE: 674575-2001
; CURRENT APPLICATION NUMBER: US/10/346,863
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: PCT/GB01/03318
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: GB 0018126.3
; PRIOR FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: GB 0025447.4
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-346-863-57

Query Match 40.9%; Score 419; DB 15; Length 192;
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[illegible]

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:29:18 ; Search time 43 Seconds
(without alignments)
343.733 Million cell updates/sec

Title: US-09-647-544-2_COPY_140_337

Perfect score: 1025

Sequence: 1 GICARVDASFPQGS LAPTA.....FLREIRTIASDPDERFFNV 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 392136

Minimum DB seq length: 0

Maximum DB seq length: 198

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	148	14.4	181	5	PCT-US96-01314-61
2	148	14.4	184	3	US-08-974-899-7
3	148	14.4	184	4	US-09-795-798-7
4	147	14.3	187	2	US-08-177-109A-62
5	147	14.3	187	2	US-08-687-706-62
6	147	14.3	187	5	PCT-US96-01314-60
7	145	14.1	184	3	US-08-974-899-8
8	145	14.1	184	4	US-09-795-798-8
9	144	14.0	187	2	US-08-177-109A-61
10	144	14.0	187	2	US-08-687-706-61
11	93	9.1	187	3	US-08-463-682-1
12	73	7.1	77	4	US-09-513-999C-6277
13	69	6.7	167	4	US-09-252-991A-21325
14	69	6.7	176	4	US-09-704-139-2
15	68.5	6.7	177	4	US-09-252-991A-29795
16	68.5	6.7	191	4	US-09-902-540-10334
17	68	6.6	188	4	US-09-902-540-10761
18	67.5	6.6	45	1	US-08-462-128-38
19	67.5	6.6	45	1	US-08-463-180-38
20	66	6.4	164	4	US-09-902-540-9764
21	65	6.3	190	4	US-09-134-000C-4833
22	64.5	6.3	180	4	US-09-904-615-78
23	64	6.2	178	4	US-09-270-767-36123
24	64	6.2	178	4	US-09-270-767-36123
25	64	6.2	182	4	US-09-270-767-61623
26	64	6.2	184	4	US-09-328-352-5086
27	63.5	6.2	85	1	US-08-341-219-22

28	63.5	6.2	85	3	US-08-912-314A-22	Sequence 22, Appl
29	63	6.1	169	4	US-09-902-540-12480	Sequence 12480, A
30	62.5	6.1	121	4	US-09-640-211A-683	Sequence 683, App
31	62	6.0	147	4	US-09-543-681A-7548	Sequence 7548, Ap
32	62	6.0	153	4	US-09-540-236-3643	Sequence 3643, Ap
33	61	6.0	193	4	US-09-252-991A-16942	Sequence 16942, A
34	61	6.0	193	4	US-09-270-767-57892	Sequence 57892, A
35	61	6.0	193	4	US-09-270-767-58950	Sequence 58950, A
36	60.5	5.9	75	3	US-08-864-357F-3	Sequence 3, Appl
37	60.5	5.9	81	4	US-09-270-767-62180	Sequence 62180, A
38	60.5	5.9	164	4	US-09-107-532A-4391	Sequence 4391, Ap
39	60	5.9	140	4	US-09-270-767-32498	Sequence 32498, A
40	60	5.9	140	4	US-09-270-767-47715	Sequence 47715, A
41	59.5	5.8	149	4	US-09-513-999C-4813	Sequence 4813, Ap
42	59	5.8	112	4	US-09-902-540-12386	Sequence 12386, A
43	59	5.8	157	4	US-09-902-540-16670	Sequence 16670, A
44	59	5.8	190	4	US-09-252-991A-32444	Sequence 32444, A
45	59	5.8	195	4	US-09-902-540-15448	Sequence 15448, A

ALIGNMENTS

RESULT 1
PCT-US96-01314-61
; Sequence 61, Application PC/TUS9601314
; GENERAL INFORMATION:
; APPLICANT: M. Amin Arnaut
; TITLE OF INVENTION: METHODS FOR IDENTIFYING INTEGRIN
; TITLE OF INVENTION: ANTAGONISTS
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/01314
; FILING DATE: 30-JAN-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/380,167
; FILING DATE: 30-JAN-95
; ATTORNEY/AGENT INFORMATION:
; NAME: John W. Freeman
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 00786/267001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 181 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-01314-61

Query Match 14.4%; Score 148; DB 5; Length 181;
Best Local Similarity 25.4%; Pred. No. 3e-10;
Matches 44; Conservative 37; Mismatches 70; Indels 22; Gaps 6;
QY 27 MDVVILVDGSLQIP--WSEVQTFLRLVGLKFLIDPEQIQVGLVQVGSPPVHWSLGF- 83
DB 6 VDLVFLFDGSLQIP--WSEVQTFLRLVGLKFLIDPEQIQVGLVQVGSPPVHWSLGF- 83
SNTSYQFAAVQFSTYKTFDFSDYV 63

REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 36537-B2-Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 187 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-463-682-1

Query Match 9.1%; Score 93; DB 3; Length 187;
Best Local Similarity 20.7%; Pred. No. 0.0029;
Matches 38; Conservative 46; Mismatches 72; Indels 28; Gaps 6;
Qy 23 CPTVMDVIVLDGNN--SIYPWSEVQTFRLRLVGLKFLDPQIOVGLVQVGESPFHWSL 80
Db 1 CSRLLDLVFLDGGSRUSEAEFEVLFKAPVDMERLRISQKWVAVVVEYHDGSHAYIGL 60
Qy 81 GDFRTKEBEVRAAKNLSRRREGRETAKQAIMVACTEGFSQSHGGRPEAARLLVVVTDGES 140
Db 61 KDKRPSRELRIASQVKYAGSQVASTSEVLKYTLFQIFSKI--DRPEASRIALLL----- 113
Qy 141 HDGELPAALKACEAGRVTRYGIAVLGHYLRQR-----DPSSFUREIRTTASD-PD 191
Db 114 -----MASQBPQMRNFRVYV-QGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPE 163
Qy 192 ERF 195
Db 164 NKA 167

RESULT 12
US-09-513-999C-6277
Sequence 6277, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 6277
LENGTH: 77
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: 66
OTHER INFORMATION: Xaa=Cys or Gly
US-09-513-999C-6277

Query Match 7.1%; Score 73; DB 4; Length 77;
Best Local Similarity 40.0%; Pred. No. 0.25;
Matches 16; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
Qy 103 ETKTAQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHD 142
Db 3 DTHGLALVYAKELQFAEASGARPGVPKVLVWVTDGSSD 42

RESULT 13
US-09-252-991A-21325
Sequence 21325, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 21325
LENGTH: 167
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21325

Query Match 6.7%; Score 69; DB 4; Length 167;
Best Local Similarity 38.7%; Pred. No. 2.7;
Matches 29; Conservative 3; Mismatches 31; Indels 12; Gaps 3;
Qy 90 VRAAKNLSRRREGRETAKQAIMVACTEGFSQSHGGRPEAARLLVVVTDGESHDG----- 143
Db 1 VMANEOKRDEGVIEKLUVQNVRAKT-----VKGRIFAFPTALTVVGDGKRGVFGRGKA 55
Qy 144 EELPAAL-KACEAGR 157
Db 56 REVPAALQKAMEAAR 70

RESULT 14
US-09-704-139-2
Sequence 2, Application US/09704139
Patent No. 6420153
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosanna
TITLE OF INVENTION: 18232, A NOVEL DUAL SPECIFICITY PHOSPHATASE AND USES THEREFOR
FILE REFERENCE: 10448-018001
CURRENT APPLICATION NUMBER: US/09/704,139
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: US 60/185,772
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 176
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(1390)
OTHER INFORMATION: n = a, t, g, or c
US-09-704-139-2

Query Match 6.7%; Score 69; DB 4; Length 176;
Best Local Similarity 28.0%; Pred. No. 2.9;
Matches 37; Conservative 17; Mismatches 50; Indels 28; Gaps 7;
Qy 89 VVRAAKNL-----SRREGRETAKQAIMVACTEGFSQSHGGR-PEAARLLVVVTDGESHD- 142
Db 19 LVRVAPSLFLGSRAGAEEQLARAVTLCNVNSRQQPGPRAPGVAELRVFVDDPAEDL 78
Qy 143 -----GEELPAALKA-----CEAGRVTRYGIAVLGHYLRQRDPS-----SPUREI 183
Db 79 LAHLEPTCAAMEAAVRAAGGACLVYCKNGR--SRSAVCTAYLWMHRLSLAKAFQWYKSA 136
Qy 184 RTIASDPDERFF 195

Db 137 RPVA-EPNPGFW 147

RESULT 15

US-09-252-991A-29795
; Sequence 29795, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 29795
; LENGTH: 177
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29795

Query Match 6.7%; Score 68.5; DB 4; Length 177;
Best Local Similarity 24.0%; Pred. No. 3.4;
Matches 37; Conservative 14; Mismatches 62; Indels 41; Gaps 6;
Qy 67 LVQYGESPVHEWSLGDPR-----KEEVVRAAKNLSRRE-----GRETKT 106
Db 28 LPRGARPTPRGPLGGTTIOPDTALLEQQGVLLKKATARCVAQAGRGGAAGPAGAPDRG 87
Qy 107 AQAIMVACTEG-----FSQSHGGRPEAARLLVVVTGESHGHD---GEELPAALKACEAGRVT 159
Db 88 ARGGRRCRCPGGPRTLYPAGGARDPRR-----SEGRGNDPFGGELGAAQRLPGLG--- 139
Qy 160 RYGIATVGHYLRORDPSSFLREIRTTIASDPDR 193
Db 140 -----LAHQLRRRRAPALRVALLRQOQQPDHR 167

Search completed: April 6, 2005, 14:41:28
Job time : 49 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 13:33:34 ; Search time 42 Seconds
(without alignments)
80.181 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986

Perfect score: 192

Sequence: 1 YEVHPYGTLPVGPGEFKTILRVQNLGCVVVGSLI 35

Scoring table: BLOSUM62

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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 7756

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	36	18.8	26	2	S05414
3	35.5	18.5	33	2	S13863
4	35	18.2	33	2	D61563
5	35	18.2	35	2	A54257
6	34.5	18.0	35	2	B36912
7	34	17.7	35	2	PC2295
8	33	17.2	10	2	H60588
9	33	17.2	30	2	I69492
10	32	16.7	22	2	P00070
11	32	16.7	30	2	S74112
12	32	16.7	35	2	PC2296
13	32	16.7	35	2	B41161
14	31.5	16.4	35	2	AD2525
15	31	16.1	19	2	S68394
16	31	16.1	20	2	A36016
17	31	16.1	24	2	T42441
18	31	16.1	24	2	B30609
19	31	16.1	28	2	A31859
20	31	16.1	28	2	JN0366
21	31	16.1	34	2	C31514
22	30.5	15.9	35	2	PC2294
23	30.5	15.9	35	2	S18264
24	30	15.6	18	2	C32537
25	30	15.6	20	2	PL0161
26	30	15.6	22	2	D32537
27	30	15.6	27	2	C54257
28	30	15.6	28	2	S41774
29	30	15.6	28	2	I48349

30 30 15.6 33 2 A95047 hypothetical prote
31 30 15.6 34 2 H95019 hypothetical prote
32 30 15.6 35 2 PC2293 V3 domain peptide
33 29.5 15.4 27 2 A24487 aldose 1-epimerase
34 29 15.1 15 2 S08282 cytochrome P450K-2
35 29 15.1 22 2 A39269 LX-1 tumor antigen
36 29 15.1 27 2 S64717 formin binding pro
37 29 15.1 30 2 A34874 transforming prote
38 29 15.1 35 2 PC2298 V3 domain peptide
39 28.5 14.8 33 2 A60507 pepsin I (EC 3.4.2
40 28 14.6 19 2 S69153 Neb-collonostatin -
41 28 14.6 20 2 S65399 immunodeficiency v
42 28 14.6 20 2 PU0033 aldose 1-epimerase
43 28 14.6 22 2 H30608 Ig kappa chain V-I
44 28 14.6 25 2 S36378 Ig heavy chain V r
45 28 14.6 26 2 G30608 Ig kappa chain V-I

ALIGNMENTS

RESULT 1

PC2297
V3 domain peptide P4611 - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: PC2297
R;Sherefa, K.; Soenmerborg, A.; Steinbergs, J.; Saellberg, M.
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A;Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide serotyping a
A;Reference number: PC2291; MUID:95110306; PMID:7811250
A;Accession: PC2297
A;Molecule type: protein
A;Residues: 1-35 <SHE>
A;Cross-references: UNIPROT:Q77729
C;Superfamily: type B retrovirus env polyprotein

Query Match 19.3%; Score 37; DB 2; Length 35;
Best Local Similarity 46.2%; Pred. No. 1.7e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTT 20

Db 11 SIPIGGRALYTT 23

RESULT 2

S05414
steryl-sulfatase (EC 3.1.6.2), microsomal - rat (fragment)
N;Alternate names: arylsulfatase C
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Apr-1993
C;Accession: S05414
R;Kawano, J.I.; Kotani, T.; Ohtaki, S.; Minamino, N.; Matsuo, H.; Oinuma, T.; Aikawa, E.
Biochim. Biophys. Acta 997, 199-205, 1989
A;Title: Characterization of rat and human steroid sulfatases.
A;Reference number: S05414; MUID:89352671; PMID:2765556
A;Accession: S05414
A;Molecule type: protein
A;Residues: 1-26 <KAW>
C;Keywords: sulfuric ester hydrolase

Query Match 18.8%; Score 36; DB 2; Length 26;
Best Local Similarity 40.9%; Pred. No. 1.7e+02;
Matches 9; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

Qy 12 GPGEPEF-----KTTLRVQNLGCV 29

Db 4 GPGGNFLLIMADDLIGDLGXY 25

RESULT 3

S13863

A;Residues: 1-30 <SCH>
A;Cross-references: UNIPROT:P82964
A;Experimental source: haemocytes
C;Keywords: antibacterial

Query Match 16.7%; Score 32; DB 2; Length 30;
Best Local Similarity 45.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PYGTLPGVGP 15
|: ||| |
DB 8 PPRPPIGPRP 18
|: ||| |

RESULT 12
V3 domain peptide P4346 - human immunodeficiency virus type 1 (fragment)
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: PC2296
R;Sherafa, K.; Soenarborg, A.; Steinbergs, J.; Saellberg, M.
Biochem. Biophys. Res. Commun. 205, 1658-1664, 1994
A;Title: Rapid grouping of HIV-1 infection in subtypes A to E by V3 peptide sequence
A;Reference number: PC2291; MUID:95110306; PMID:7811250
A;Accession: PC2296
A;Molecule type: protein
A;Residues: 1-35 <SHE>
A;Cross-references: UNIPROT:Q70826; UNIPROT:Q70831
C;Superfamily: type E retrovirus env polyprotein

Query Match 16.7%; Score 32; DB 2; Length 35;
Best Local Similarity 46.2%; Pred. No. 8.8e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 TLPVGPGRPEKTT 20
|: ||| | | |
DB 11 SIHWGPRAFYTT 23
|: ||| | | |

RESULT 13
B41161
29K antigen PRB2 - Campylobacter jejuni (fragment)
C;Species: Campylobacter jejuni
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004
C;Accession: B41161
R;Pei, Z.; Ellison III, R.T.; Blaser, M.J.
J. Biol. Chem. 266, 16363-16369, 1991
A;Title: Identification, purification, and characterization of major antigenic
A;Reference number: A41161; MUID:91358413; PMID:1885571
A;Accession: B41161
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-35 <PEI>
A;Cross-references: UNIPROT:Q9R5T9

Query Match 16.7%; Score 32; DB 2; Length 35;
Best Local Similarity 47.1%; Pred. No. 8.8e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 2; Gaps 1;

QY 2 EVHPYGLPGVGPPEFK 18
|: ||| | | | |
DB 1 EILVYG--PGGPAPVLK 15
|: ||| | | |

RESULT 14
AD2525
hypothetical protein asr7380 [imported] - Nostoc sp. (strain PCC 7120) plasmid
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AD2525
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.;

DNA Res. 8, 205-213, 2001
A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A/Reference number: AB1807; MUID:21595285; PMID:11759840
A/Accession: AD2525
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-35 <KUR>
A/Cross-references: UNIPROT:Q8YKCL; GB:BA000020; PIDN:BA077138.1; PID:g17134579; GSPDB:G
A/Experimental source: strain PCC 7120
C/Genetics:
A/Gene: asr7380
A/Genome: plasmid

Query Match 16.4%; Score 31.5; DB 2; Length 35;
Best Local Similarity 40.7%; Pred. No. 1e+03;
Matches 11; Conservative 1; Mismatches 2; Indels 13; Gaps 2;

Qy 11 VGPPEPKTLRVQN-----LGC 28
||| |||||
Db 6 VGDG----DTLRVRNQOQPITIRLGC 28

RESULT 15

S68394
H+-transporting two-sector ATPase (EC 3.6.3.14) chain G - Chlamydomonas reinhardtii (fra
N/Alternate names: ATP synthase chain G
C/Species: Chlamydomonas reinhardtii
C/Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C/Accession: S68394
R/Fiedler, H.R.; Schmid, R.; Leu, S.; Shavit, N.; Strotmann, H.
FEBS Lett. 377, 163-166, 1995
A/Title: Isolation of CF(0)CF(1) from Chlamydomonas reinhardtii cw15 and the N-terminal
A/Reference number: S68388; MUID:96128220; PMID:8543042
A/Accession: S68394
A/Molecule type: protein
A/Residues: 1-19 <FIE>
A/Cross-references: UNIPROT:Q98882
A/Experimental source: strain CW15
C/Genetics:
A/Genome: nuclear
C/Keywords: chloroplast; hydrolase

Query Match 16.1%; Score 31; DB 2; Length 19;
Best Local Similarity 40.0%; Pred. No. 6.2e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 EVHPYGTLPVGPGE 16
::: |||
Db 4 KIDFNTLPVNAGEE 18

Search completed: April 6, 2005, 13:46:20
Job time : 43 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 13:10:34 ; Search time 180 Seconds
(without alignments)
99.571 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986

Perfect score: 192

Sequence: 1 YEVHPGTLPVGPGEFKTLRVQNLGCVVSGLI 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 37082

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	24.0	34	2 O91354	human immun
2	46	24.0	34	2 O91355	human immun
3	46	24.0	34	2 O91357	human immun
4	46	24.0	34	2 O78489	human immun
5	45	23.4	34	2 O78487	human immun
6	45	23.4	35	2 O90519	human immun
7	45	23.4	35	2 O91436	human immun
8	45	23.4	35	2 O91437	human immun
9	45	23.4	35	2 O76251	human immun
10	44	22.9	35	2 O10859	human immun
11	44	22.9	35	2 O91434	human immun
12	44	22.9	35	2 O91454	human immun
13	44	22.9	35	2 Q6W884	human immun
14	44	22.9	35	2 O76250	human immun
15	44	22.9	35	2 O76236	human immun
16	44	22.9	35	2 O80499	human immun
17	43	22.4	34	2 O91356	human immun
18	43	22.4	34	2 O6QP03	human immun
19	43	22.4	34	2 Q70742	human immun
20	43	22.4	34	2 Q70743	human immun
21	43	22.4	34	2 Q70747	human immun
22	43	22.4	35	2 O90503	human immun
23	43	22.4	35	2 O91349	human immun
24	43	22.4	35	2 O91350	human immun
25	43	22.4	35	2 O91351	human immun
26	43	22.4	35	2 O91430	human immun
27	43	22.4	35	2 O91433	human immun
28	43	22.4	35	2 O91435	human immun
29	43	22.4	35	2 O91438	human immun
30	43	22.4	35	2 O91439	human immun
31	43	22.4	35	2 O91440	human immun

32	43	22.4	35	2 O91446	human immun
33	43	22.4	35	2 Q6W882	human immun
34	43	22.4	35	2 Q6W892	human immun
35	43	22.4	35	2 Q6W893	human immun
36	43	22.4	35	2 Q6W894	human immun
37	43	22.4	35	2 Q70232	human immun
38	43	22.4	35	2 Q76295	human immun
39	43	22.4	35	2 Q76PL9	human immun
40	43	22.4	35	2 Q76PM0	human immun
41	43	22.4	35	2 Q76PM1	human immun
42	43	22.4	35	2 Q76PM2	human immun
43	43	22.4	35	2 Q76PM3	human immun
44	43	22.4	35	2 Q76PM4	human immun
45	43	22.4	35	2 Q76PM5	human immun

ALIGNMENTS

RESULT 1

O91354 ID O91354 PRELIMINARY; PRT; 34 AA.
AC O91354;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090117; PubMed=9430252;
RA Ida S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,
RA Kimura S., Iwamoto A., Oka S.;
RT "HIV type 1 V3 variation dynamics in vivo: long-term persistence of
RT non-syncytium-inducing genotypes and transient presence of syncytium-
RT inducing genotypes during the course of progressive AIDS.";
RL AIDS Res. Hum. Retroviruses 13:1597-1609 (1997).
DR EMBL; AB005326; BAA3244.1;
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR00777; GP120.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 3785 MW; A31972064FAD828F CRC64;

Query Match 24.0%; Score 46; DB 2; Length 34;

Best Local Similarity 42.1%; Pred. No. 61;

Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Oy 8 TLPVGPGEFKTLRVQNL 26

:::|||||:::

Db 11 SIPIGPGAFYTTIIGNI 29

RESULT 2

O91355 ID O91355 PRELIMINARY; PRT; 34 AA.
AC O91355;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.


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RL Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; M92127; AAA44575.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane.
FT NON_TER 1 34
FT NON_TER 34 34
SQ SEQUENCE 34 AA; 3818 MW; A93F02E148C0428F CRC64;

Query Match 23.4%; Score 45; DB 2; Length 34;
Best Local Similarity 42.1%; Pred. No. 85;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTTLRVNL 26
Db 11 SIPMGPGAFYTTIIGNI 29

RESULT 6
ID O90519 PRELIMINARY; PRT; 35 AA.
AC O90519;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99211246; PubMed=10197389;
RA Vallejo A., Mas A., Heredia A., Altisent C., Lorenzo I., Soriano V.,
RA Hewlett I.K.;
RT "V3-loop and nef gene sequences of HIV-1 isolates from a hemophilic
RT cohort with long-term non-progressive infection.";
RL AIDS 13:532-534(1999).
DR EMBL; AF082373; AAC34519.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3878 MW; 9F5A59F6B78C81BE CRC64;

Query Match 23.4%; Score 45; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTTLRV 23
Db 11 SIPMGPGAFYTTDRI 26

RESULT 7
ID O91436 PRELIMINARY; PRT; 35 AA.
AC O91436;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99211246; PubMed=10197389;
RA Vallejo A., Mas A., Heredia A., Altisent C., Lorenzo I., Soriano V.,
RA Hewlett I.K.;
RT "V3-loop and nef gene sequences of HIV-1 isolates from a hemophilic
RT cohort with long-term non-progressive infection.";
RL AIDS 13:532-534(1999).
DR EMBL; AF082373; AAC34519.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3878 MW; 9F5A59F6B78C81BE CRC64;

Query Match 23.4%; Score 45; DB 2; Length 35;
Best Local Similarity 50.0%; Pred. No. 87;
Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTTLRV 23
Db 11 SIPMGPGAFYTTDRI 26

RESULT 7
ID O91436 PRELIMINARY; PRT; 35 AA.
AC O91436;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99211246; PubMed=10197389;
RA Vallejo A., Mas A., Heredia A., Altisent C., Lorenzo I., Soriano V.,
RA Hewlett I.K.;
RT "V3-loop and nef gene sequences of HIV-1 isolates from a hemophilic
RT cohort with long-term non-progressive infection.";
RL AIDS 13:532-534(1999).
DR EMBL; AF082373; AAC34519.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3878 MW; 9F5A59F6B78C81BE CRC64;
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GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090117; PubMed=9430252;
RA Ida S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,
RA Kimura S., Iwamoto A., Oka S.;
RT "HIV type 1 V3 variation dynamics in vivo: long-term persistence of
RT non-syncytium-inducing genotypes and transient presence of syncytium-
RT inducing genotypes during the course of progressive AIDS.";
RL AIDS Res. Hum. Retroviruses 13:1597-1609(1997).
DR EMBL; AB005421; BAA33338.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3956 MW; 9F5A5B3A688BF77E CRC64;

Query Match 23.4%; Score 45; DB 2; Length 35;
Best Local Similarity 43.8%; Pred. No. 87;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTTLRV 23
Db 11 SIPMGPGAFYTTROI 26

RESULT 8
ID O91437 PRELIMINARY; PRT; 35 AA.
AC O91437;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98090117; PubMed=9430252;
RA Ida S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,
RA Kimura S., Iwamoto A., Oka S.;
RT "HIV type 1 V3 variation dynamics in vivo: long-term persistence of
RT non-syncytium-inducing genotypes and transient presence of syncytium-
RT inducing genotypes during the course of progressive AIDS.";
RL AIDS Res. Hum. Retroviruses 13:1597-1609(1997).
DR EMBL; AB005422; BAA33339.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR InterPro; IPR011056; Pept_S24_S26_C.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1 35
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3956 MW; 9F5A5B3A688BF77E CRC64;

Query Match 23.4%; Score 45; DB 2; Length 35;
Best Local Similarity 43.8%; Pred. No. 87;
Matches 7; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```



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RN  SEQUENCE FROM N.A.
RP  MEDLINE=98090117; PubMed=9430252;
RA  Ida S., Gatanaga H., Shioda T., Nagai Y., Kobayashi N., Shimada K.,
RA  Kimura S., Iwamoto A., Oka S.;
RT  "HIV type 1 V3 variation dynamics in vivo: long-term persistence of
RT  non-synctium-inducing genotypes and transient presence of cyncytium-
RT  inducing genotypes during the course of progressive AIDS.";
RL  AIDS Res. Hum. Retroviruses 13:1597-1609 (1997).
DR  EMBL; AB005440; BAA33356.1; -
DR  GO; GO:0016021; C: integral to membrane; IEA.
DR  GO; GO:0019028; C: viral capsid; IEA.
DR  GO; GO:0019031; C: viral envelope; IEA.
DR  GO; GO:0005198; F: structural molecule activity; IEA.
DR  InterPro; IPR000777; GP120.
DR  Pfam; PF00516; GP120; 1.
DR  AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
KW  AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT  NON_TER 1
FT  NON_TER 35
SQ  SEQUENCE 35 AA; 4026 MW; 9E4A4A3A688BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LPVGPGEFKTTLRV 23
Db 12 IPIGPGAFYTTQI 26

RESULT 13
ID Q6W884 PRELIMINARY; PRT; 35 AA.
AC Q6W884;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE GP120 (Fragment).
OS Name=env;
GN Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22918189; PubMed=14554089; DOI=10.1016/S0042-6822(03)00464-1;
RA Kulkosky J., Sullivan J., Xu Y., Malin-Markham A., Otero M.,
RA Calarota S., Zielinski J., Culnan D.M., Pomerantz R.J.;
RT "Genotypic alteration of HAART-persistent HIV-1 reservoirs in vivo.";
RL Virology 314:617-629 (2003).
DR EMBL; AY305414; AAQ88346.1; -
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3830 MW; 9F48FD8B88BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 8 TLPVGPGEFKTT 20
Db 11 SIPIGPGAFYTT 23

RESULT 14
Q76250
ID Q76250 PRELIMINARY; PRT; 35 AA.
AC Q76250;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE V3 loop (Fragment).
OS Name=env;
GN Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94246736; PubMed=8189527;
RA Schreiber M.G., Petersen H., Wachsmuth C., Muller H., Hufert F.T.,
RA Schmitz H.;
RT "Antibodies of symptomatic human immunodeficiency virus type 1-
RT infected individuals are directed to the V3 domain of noninfectious
RT and not of infectious virions present in autologous serum.";
RL J. Virol. 68:3908-3916 (1994).
DR EMBL; Z15163; CAA78862.1; -
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3775 MW; 9F5B905B698BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LPVGPGEFKTTLRV 23
Db 12 IPIGPGAFYTTQI 26

RESULT 15
Q76296
ID Q76296 PRELIMINARY; PRT; 35 AA.
AC Q76296;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE V3 loop (Fragment).
OS Name=env;
GN Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94246736; PubMed=8189527;
RA Schreiber M.G., Petersen H., Wachsmuth C., Muller H., Hufert F.T.,
RA Schmitz H.;
RT "Antibodies of symptomatic human immunodeficiency virus type 1-
RT infected individuals are directed to the V3 domain of noninfectious
RT and not of infectious virions present in autologous serum.";
RL J. Virol. 68:3908-3916 (1994).
DR EMBL; Z15163; CAA78862.1; -
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3775 MW; 9F5B905B698BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LPVGPGEFKTTLRV 23
Db 12 IPIGPGAFYTTQI 26
```

```

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE V3 loop (fragment).
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Schreiber M.G.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z50844; CAA90697.1; -
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein; Transmembrane.
KW AIDS; Coat protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3898 MW; 8A1B0F25558BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LPVGPGEFKTTLRV 23
Db 12 IPIGPGAFYTTQI 26

RESULT 15
Q76296
ID Q76296 PRELIMINARY; PRT; 35 AA.
AC Q76296;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE V3 loop (Fragment).
OS Name=env;
GN Human immunodeficiency virus 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=94246736; PubMed=8189527;
RA Schreiber M.G., Petersen H., Wachsmuth C., Muller H., Hufert F.T.,
RA Schmitz H.;
RT "Antibodies of symptomatic human immunodeficiency virus type 1-
RT infected individuals are directed to the V3 domain of noninfectious
RT and not of infectious virions present in autologous serum.";
RL J. Virol. 68:3908-3916 (1994).
DR EMBL; Z15163; CAA78862.1; -
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0019028; C: viral capsid; IEA.
DR GO; GO:0019031; C: viral envelope; IEA.
DR GO; GO:0005198; F: structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein; Transmembrane.
FT NON_TER 1
FT NON_TER 35
SQ SEQUENCE 35 AA; 3775 MW; 9F5B905B698BF77E CRC64;

Query Match 22.9%; Score 44; DB 2; Length 35;
Best Local Similarity 53.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LPVGPGEFKTTLRV 23
Db 12 IPIGPGAFYTTQI 26
```

Qy 8 TLPVGPGEFKTT 20
: : : : :
Db 11 SIPIGGSFYTT 23

Search completed: April 6, 2005, 13:44:42
Job time : 181 secs

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OM protein - protein search, using sw model

Run on: April 6, 2005, 13:08:44 ; Search time 168 Seconds
(without alignments)
80.575 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986
Perfect score: 192
Sequence: 1 YEHVPVGTLPVGPGEKFTLRVQNLGCVVSGLI 35

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 854512

Minimum DB seq length: 0
Maximum DB seq length: 35

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	24.0	33	2 AAR68713	PRI/T5 ch
2	46	24.0	33	2 AAW25883	Chimaeric
3	46	24.0	33	2 AAW67399	AAW67399 HIV-1 pep
4	46	24.0	33	2 AAW98900	AAW98900 HIV-1 vac
5	46	24.0	33	2 AAY39728	AAy39728 HIV1 chim
6	46	24.0	35	2 AAR77763	PRI/T5 ch
7	45.5	23.7	33	2 AAR68712	AAr68712 T5/PRI ch
8	45.5	23.7	33	2 AAW25882	Chimaeric
9	45.5	23.7	33	2 AAW67398	AAW67398 HIV-1 pep
10	45.5	23.7	33	2 AAW98899	AAW98899 HIV-1 vac
11	45.5	23.7	33	2 AAY39727	AAy39727 HIV1 chim
12	45.5	23.7	35	2 AAR77762	T5/PRI ch
13	44	22.9	24	2 AAR04467	Human imm
14	44	22.9	35	3 AAB10706	ABg10706 HIV-1 iso
15	44	22.9	35	5 AEG73686	ABg73686 HIV-1 V3-
16	43.5	22.7	33	2 AAR68710	PRI/P24H
17	43.5	22.7	33	2 AAW25880	Chimaeric
18	43.5	22.7	33	2 AAW67396	AAW67396 HIV-1 pep
19	43.5	22.7	33	2 AAW98897	AAW98897 HIV-1 vac
20	43.5	22.7	33	2 AAY39725	AAy39725 HIV1 chim
21	43.5	22.7	35	2 AAR77760	PRI/P24H
22	43	22.4	18	2 AAR68679	Consensus
23	43	22.4	18	2 AAY04445	Peptide C
24	43	22.4	18	2 AAW25849	env
25	43	22.4	18	2 AAW67365	HIV-1 V3

26	43	22.4	18	2 AAW99973	AAw99973 HIV-1 vac
27	43	22.4	18	2 AAY39698	AAy39698 HIV1 chim
28	43	22.4	24	2 AAR38170	V3 loop p
29	43	22.4	33	2 AAR68709	AAr68709 P24H/PRI
30	43	22.4	33	2 AAR68670	AAr68670 p24E/V3 c
31	43	22.4	33	2 AAW25879	Chimaeric
32	43	22.4	33	2 AAW25840	Chimaeric
33	43	22.4	33	2 AAW67395	AAw67395 HIV-1 pep
34	43	22.4	33	2 AAW67356	AAw67356 HIV-1 pep
35	43	22.4	33	2 AAW98896	AAw98896 HIV-1 vac
36	43	22.4	33	2 AAY39724	AAy39724 HIV-1 vac
37	43	22.4	33	2 AAY39724	HIV1 chim
38	43	22.4	33	2 AAY39762	AAy39762 HIV1 chim
39	43	22.4	34	2 AAR68674	Chimaeric
40	43	22.4	34	2 AAW25844	Chimaeric
41	43	22.4	34	2 AAW67360	AAW67360 HIV-1 pep
42	43	22.4	34	2 AAW99968	AAW99968 HIV-1 vac
43	43	22.4	34	2 AAY39765	AAy39765 HIV1 chim
44	43	22.4	35	2 AAR21089	PND EE15-
45	43	22.4	35	2 AAR21090	PND EE15-

ALIGNMENTS

RESULT 1

AAAR68713	ID	AAAR68713	standard; peptide; 33 AA.
AC	AAAR68713;		
AC	AAAR68713;		
DT	16-OCT-2003 (revised)		
DT	25-MAR-2003 (revised)		
DT	07-SEP-1995 (first entry)		
XX	XX		
DE	PRI/T5 chimera, CLTB-159.		
XX	XX		
KW	T-cell; epitope; HIV-1; core protein; p24E; B-cell; antigen; gp160; gag;		
KW	pol; vaccine; multimeric peptide; AIDS; 3D organisation.		
XX	XX		
OS	Human immunodeficiency virus 1.		
XX	XX		
PH	Key	Location/Qualifiers	
FT	Peptide	1..18	
FT	FT	/label= PRI	
FT	FT	/note= "B cell epitope"	
FT	Peptide	19..33	
FT	FT	/label= T5	
FT	FT	/note= "T cell epitope"	

WO9429339-A1.

22-DEC-1994.

08-JUN-1994; 94WO-CA000317.

09-JUN-1993; 93US-00073378.

(CONN-) CONNAUGHT LAB LTD.

Sia CDY, Chong P, Klein MH;

WPI, 1995-036400/05.

Novel tandem synthetic HIV-1 peptide(s) - comprising T-cell epitope of gag protein linked to B-cell epitope of V3 loop protein of an HIV-1 isolate.

Claim 4; Page 46; 69pp; English.

This sequence represents the T-cell epitope derived from the HIV-1 core protein, T5, linked to a B-cell epitope, PRI which represents a consensus sequence derived from New York and Amsterdam HIV-1 isolates. Chimeric

[illegible]

XX The invention relates to new synthetic peptides comprising at least one
CC amino acid sequence comprising an HIV gag protein T-cell epitope linked
CC at its C- or N-terminus to an amino acid sequence comprising a B-cell
CC epitope of the V3 loop of an HIV env protein, which can be used to
CC generate vaccines against HIV-1. The T-cell epitope sequence is pref.
CC selected from the T-helper determinant core peptides P24E, P24N, P24L,
CC P24M and P24H while the B-cell epitopes are derived from HIV strains
CC including CTLB-56, V3MN, CTLB-29, CTLB-55, SF2, LAI, IIB, RF, Z6, 2054,
CC 1714 and BX08. The peptides are chimeric and can be linked to a branched
CC lys backbone. This sequence represents a chimeric peptide comprising the
CC T-helper determinant core peptide T5 (AAW25881) with the HIV-1 strain MN
CC env protein V3 loop B-cell epitope PRI which corresponds to a peptide
CC generated from the consensus sequence of the New York and Amsterdam HIV-1
CC isolates. The B-cell epitope is linked to the C-terminus of the T-helper
CC peptide. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 33 AA;

Query Match 23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 81;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPVGPGEFKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 9
AAW67398
ID AAW67398 standard; peptide; 33 AA.
XX
AC AAW67398;
XX
XX 25-JAN-1999 (first entry)
XX
DE HIV-1 peptide epitope CTLB-158.
XX
KW Immunogen; vaccine; HIV-1; T-cell; B-cell; epitope; core protein; gp120;
KW V3 loop.
XX
OS Synthetic.
OS Human immunodeficiency virus 1.
XX
XX US5817754-A.
XX
XX 06-OCT-1998.
XX
XX 05-JUN-1995; 95US-00464329.
XX
PR 09-JUN-1993; 93US-00073378.
PR 09-JUN-1994; 94US-00257528.
XX
PA (CONN-) CONNAUGHT LAB LTD.
XX
PI Chong P, Klein MH, Sia CDY;
XX
DR WPI; 1998-556461/47.
XX
XX Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell
PT epitope and B-cell epitope(s) are candidate vaccines against HIV-1.
XX
PS Disclosure; Col 23-24; 40pp; English.
XX
XX The invention relates to a novel immunogenic composition for use in
CC vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell
CC epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes
CC are generally designed based on the p24 core protein and the B-cell
CC epitopes from the V3 loop of the gp120 protein from various HIV-1
CC strains. This peptide corresponds to a fusion of the T5 epitope
CC (AAW67397) and the V3 loop B-cell epitope (AAW67365) which is a consensus
CC V3 loop peptide of the New York and Amsterdam HIV-1 isolates
XX

SQ Sequence 33 AA;

Query Match 23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 81;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPVGPGEFKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 10
AAW98899
ID AAW98899 standard; peptide; 33 AA.
XX
AC AAW98899;
XX
XX 05-MAY-1999 (first entry)
XX
DE HIV-1 vaccine synthetic peptide SEQ ID NO:83.
XX
KW HIV-1; human immunodeficiency virus; vaccine; T-cell epitope;
KW gag protein; B-cell epitope; gp41 protein; chimeric; infection.
XX
OS Synthetic.
OS Human immunodeficiency virus 1.
XX
XX US5876731-A.
XX
XX 02-MAR-1999.
XX
PF 05-JUN-1995; 95US-00462507.
XX
PR 09-JUN-1993; 93US-00073378.
PR 09-JUN-1994; 94US-00257528.
XX
XX (CONN-) CONNAUGHT LAB LTD.
XX
XX Chong P, Klein MH, Sia CDY;
XX
XX WPI; 1999-189590/16.
XX
XX Synthetic chimeric HIV polypeptides - comprising gag protein T-cell
PT epitope linked to gp41 B-cell epitope.
XX
XX Example 1; Col 63-64; 41pp; English.
XX
XX The present invention describes a synthetic peptide comprising an amino
CC acid sequence containing a T-cell epitope of an HIV gag protein linked at
CC its C terminus to an amino acid sequence containing a B-cell epitope of
CC an HIV gp41 protein and containing the amino acid sequence: X1LKDWX2;
CC where X1 = E, A, G or Q, and X2 = A or T, or an amino acid sequence
CC capable of eliciting an HIV-specific antiserum and recognizing the
CC sequence X1LKDWX2. The synthetic peptide is useful in vaccines against
CC HIV infection and in diagnostic applications. AAW98892 to AAW98906, and
CC AAW98999 to AAW99989 represent synthetic peptides from the present
CC invention
XX
SQ Sequence 33 AA;

Query Match 23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 81;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPVGPGEFKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 11
AAV39727
ID AAV39727 standard; peptide; 33 AA.
XX

KW HIV isolate AVR-2; peptide RP150; principal neutralising domain;
 KW antibodies; diagnosis; prophylaxis; therapy; AIDS.
 OS Synthetic.
 XX WO9003984-A.
 XX
 XX 19-APR-1990.
 XX
 XX 03-OCT-1988; 88US-00252949.
 XX
 XX 03-OCT-1988; 88US-00252949.
 XX
 XX 01-JUN-1989; 89US-00359543.
 XX
 XX 19-SEP-1989; 89US-00407663.
 XX
 XX (REPK) REPLIGEN CORP.
 XX
 XX Rusche JR, Putney SD, Javaherian K, Farley J, Grimailla R;
 PI Lynn DU, Petrobre J;
 XX WPI; 1990-147824/19.
 XX
 XX Principal neutralising domain of HIV variants - used for producing
 PT peptide(s) and antibodies for diagnosis, prophylaxis and/or therapy
 PT therapy of HIV infection.
 XX
 XX Claim 8 (81); Page 77; 108pp; English.
 XX
 XX Peptide RP150 comprises segments of the Principal Neutralising Domain
 CC (envelope protein) from isolate AVR-2. The last Cys residue is added for
 CC the purpose of crosslinking to carrier proteins. Cysteine residues may be
 CC added, so that the residues at or near both ends form a disulfide bond,
 CC giving peptide a loop-like configuration, which can be utilised to
 CC enhance the immunogenic properties of the peptides. Protein is capable of
 CC eliciting, and/or binding with, neutralising Abs. The neutralising domain
 CC is bounded by cysteine residues which occur at positions 296 and 331.
 CC Peptides can be used as immunogens or screening reagents to generate or
 CC identify poly- or monoclonal antibodies. See also AAR0427-R04506 and
 CC AAQ04273-004279. (Updated on 25-MAR-2003 to correct PR field.) (Updated
 CC on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct
 CC PI field.)
 CC
 CC Revised record issued on 09-SEP-2004 : Correction to Feature Table Key
 XX
 XX Sequence 24 AA;
 Qy Best Match 22.9%; Score 44; DB 2; Length 24;
 Best Local Similarity 50.0%; Pred. No. 93;
 Matches 9; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
 Qy 11 VGPGEPEKTLRVQNLGC 28
 :||| :||| :|||
 Db 9 IGPGRFHTTGRI--IGC 24
 :||| :||| :|||
 RESULT 14
 ID AAB10706 standard; protein; 35 AA.
 XX
 XX AAB10706;
 XX
 XX 12-SEP-2003 (revised)
 DT 26-JAN-2001 (first entry)
 XX
 XX HIV-1 isolate PI-932 gp120 protein V3 loop region fragment.
 XX
 XX Viral protein; vaccine; anti-viral; anti-HIV; therapy; infection; gp120;
 KW V3 loop.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX WO200047223-A2.
 PN
 XX

PD 17-AUG-2000.
 XX
 XX 03-DEC-1999; 99WO-EP009759.
 XX
 XX 12-FEB-1999; 99DE-01007485.
 XX
 XX (STRA-) STRATHMANN & CO AG.
 XX
 XX Schreiber M;
 PI
 XX WPI; 2000-549084/50.
 DR
 XX
 XX Viral vaccine comprises a mixture of protein sequence variants of a
 PT single viral protein, which is useful for prevention and therapy of viral
 PT infections, especially HIV, in humans.
 XX
 XX Disclosure; Fig 1; 79pp; German.
 PS
 XX This invention describes a novel protein vaccine which comprises a
 CC mixture of viral proteins, characterized in that the molecules are
 CC sequence variants of a single viral (partial) protein. The products of
 CC the invention have anti-viral and anti-HIV activity. Mixtures of
 CC structurally different viral proteins, that are sequence variants of a
 CC single protein are useful for production of vaccines for the prevention
 CC and/or therapy of viral infections in humans. The vaccines are especially
 CC useful for prevention and/or therapy of human immunodeficiency virus
 CC (HIV) infection in humans. The vectors and host cells are useful for the
 CC expression of the protein/DNA mixtures, which are also useful for
 CC preventing and/or therapy of viral infection. This sequence represents a
 CC gp120 protein V3 loop fragment from HIV-1 isolate PI-932. (Updated on 12-
 CC SEP-2003 to standardise OS field)
 XX
 XX Sequence 35 AA;
 SQ
 Qy Best Match 22.9%; Score 44; DB 3; Length 35;
 Best Local Similarity 30.8%; Pred. No. 1.4e+02;
 Matches 8; Conservative 7; Mismatches 7; Indels 4; Gaps 1;
 Qy 3 VHPYGT----LPVGPGEPEKTLRVQ 24
 :||| :||| :||| :|||
 Db 2 IRPHNTVTDRIHIGGRSFHTTRKIK 27
 :||| :||| :||| :|||
 RESULT 15
 ID ABG73686 standard; peptide; 35 AA.
 XX
 XX ABG73686;
 XX
 XX 29-AUG-2003 (revised)
 DT 11-MAR-2003 (first entry)
 XX
 XX HIV-1 V3-loop region (CXCR4-type) from isolate PI-932.
 XX
 XX gp120; interaction; co-receptor; CXCR4; CCR5; refractive index; V3 loop;
 KW 7-helix transmembrane receptor; glycopeptide; virucide; anti-HIV;
 KW HIV infection.
 XX
 XX Human immunodeficiency virus 1.
 OS
 XX DE10113042-A1.
 XX
 XX 26-SEP-2002.
 PD
 XX
 XX 09-MAR-2001; 2001DE-01013042.
 PF
 XX 09-MAR-2001; 2001DE-01013042.
 XX
 XX (NOCH-) NOCHT INST TROPENMEDIZIN BERNHARD.
 XX
 XX Schreiber M, Seifert A, Meyer B;
 PI
 XX WPI; 2002-752120/82.
 DR

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OM protein - protein search, using sw model

Run on: April 6, 2005, 13:44:50 ; Search time 139 Seconds
(without alignments)
83.596 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986

Perfect score: 192

Sequence: 1 YEVHPVGTLPVGPGEKTLRVQNLGCVVSGLI 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 361004

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44.5	23.2	35	US-10-424-599-185421	Sequence 185421,
2	43.5	22.7	28	US-10-443-622-133	Sequence 133, App
3	42	21.9	29	US-10-106-698-7462	Sequence 7462, Ap
4	42	21.9	35	US-10-424-599-238025	Sequence 238025,
5	40	20.8	23	US-10-125-869A-148	Sequence 148, App
6	40	20.8	23	US-10-462-262-372	Sequence 372, App
7	40	20.8	24	US-10-080-608A-71	Sequence 71, Appl
8	40	20.8	24	US-10-371-067-2	Sequence 2, Appl1
9	39	20.3	20	US-09-864-761-39770	Sequence 39770, A
10	39	20.3	21	US-09-864-761-46555	Sequence 46555, A
11	39	20.3	23	US-09-843-676-208	Sequence 208, App
12	39	20.3	23	US-09-438-486-208	Sequence 208, App
13	39	20.3	23	US-10-053-758-208	Sequence 208, App

14	39	20.3	23	14	US-10-054-295-208	Sequence 208, App
15	39	20.3	23	14	US-10-054-611-208	Sequence 208, App
16	39	20.3	23	15	US-10-325-810-327	Sequence 327, App
17	39	20.3	23	17	US-10-877-146-327	Sequence 327, App
18	39	20.3	24	10	US-09-798-889-167	Sequence 167, App
19	39	20.3	24	15	US-10-633-680-167	Sequence 167, App
20	39	20.3	35	10	US-09-759-947C-14	Sequence 14, Appl
21	38	19.8	15	9	US-09-810-310-27	Sequence 27, Appl
22	38	19.8	23	17	US-10-621-675-155	Sequence 155, App
23	38	19.8	24	10	US-09-933-767-472	Sequence 472, App
24	38	19.8	24	14	US-10-004-860-472	Sequence 472, App
25	38	19.8	24	14	US-10-023-283-472	Sequence 472, App
26	38	19.8	29	14	US-10-045-465-12	Sequence 12, Appl
27	38	19.8	33	14	US-10-272-339A-18	Sequence 18, Appl
28	38	19.8	33	14	US-10-272-339A-20	Sequence 20, Appl
29	37.5	19.5	30	15	US-10-057-475B-10828	Sequence 10828, A
30	37.5	19.5	30	15	US-10-154-884B-10828	Sequence 10828, A
31	37	19.3	16	15	US-10-285-394-183	Sequence 183, App
32	37	19.3	16	15	US-10-601-837-104	Sequence 104, App
33	37	19.3	16	15	US-10-601-837-105	Sequence 105, App
34	37	19.3	34	17	US-10-628-004-13	Sequence 13, Appl
35	36.5	19.0	27	11	US-09-833-245-1258	Sequence 1258, Ap
36	36.5	19.0	28	10	US-09-892-877-293	Sequence 293, App
37	36.5	19.0	28	10	US-09-948-783-305	Sequence 305, App
38	36	18.8	15	9	US-09-810-310-28	Sequence 28, Appl
39	36	18.8	15	14	US-10-320-175-7	Sequence 7, Appl
40	36	18.8	15	17	US-10-701-682A-373	Sequence 373, App
41	36	18.8	17	10	US-09-964-201A-3	Sequence 3, Appl1
42	36	18.8	17	14	US-10-161-791-331	Sequence 331, App
43	36	18.8	17	16	US-10-681-389-3	Sequence 3, Appl1
44	36	18.8	17	16	US-10-681-388-3	Sequence 3, Appl1
45	36	18.8	22	10	US-09-932-13844C.1	Sequence 167, App

ALIGNMENTS

RESULT 1

US-10-424-599-185421
; Sequence 185421, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 185421
; LENGTH: 35
; TYPE: PRI
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_13844C.1.pep
US-10-424-599-185421

Query Match 23.2%; Score 44.5; DB 15; Length 35;
Best Local Similarity 52.9%; Pred. No. 1.1e+02;
Matches 9; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 17 FKTLRVQNLG-CYVWS 32

Db 10 YNTTARVDNLGDCYTLLA 26

RESULT 2

US-10-443-622-133
; Sequence 133, Application US/10443622
; Publication No. US20040024192A1

GENERAL INFORMATION:
; APPLICANT: Carter et al.
; TITLE OF INVENTION: 19 Human Secreted Proteins
; FILE REFERENCE: P2009P1
; CURRENT APPLICATION NUMBER: US/10/443,622
; CURRENT FILING DATE: 2003-05-23
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: PCT/US98/13608
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 60/051,480
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 60/051,381
; PRIOR FILING DATE: 1997-07-01
; PRIOR APPLICATION NUMBER: 60/058,663
; PRIOR FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: 60/058,598
; PRIOR FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 156
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 133
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-443-622-133

Query Match 22.7%; Score 43.5; DB 15; Length 28;
Best Local Similarity 42.1%; Pred. No. 1.1e+02;
Matches 8; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

Qy 4 HPYGTLPVGPQPEPKTTLR 22
Db 7 HPVSS-PEGPQVYRGARR 24

RESULT 3
US-10-106-598-7462
; Sequence 7462, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR FILING DATE: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 7462
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (6)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: MISC FEATURE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-598-7462

Query Match 21.9%; Score 42; DB 14; Length 29;
Best Local Similarity 56.2%; Pred. No. 1.9e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

Qy 4 HPYGTLPVGPQPEF 17
Db 11 HYFGKLVPPAGTGPPEF 26

RESULT 4
US-10-424-599-238025
; Sequence 238025, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 238025
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_56963C.1.pap
US-10-424-599-238025

Query Match 21.9%; Score 42; DB 15; Length 35;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 PVGPGPEPKT 19
Db 4 PAGPGPVFNT 13

RESULT 5
US-10-125-869A-148
; Sequence 148, Application US/10125869A
; Publication No. US20030199671A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac Jesus
; APPLICANT: Wu, Oi-Long
; APPLICANT: Ley, Arthur C.
; APPLICANT: Stochl, Mark
; APPLICANT: Ransohoff, Thomas C.
; APPLICANT: Potter, M. Daniel (deceased)
; TITLE OF INVENTION: BINDING MOLECULES FOR FC-REGION
; FILE REFERENCE: 3421.1006-001
; CURRENT APPLICATION NUMBER: US/10/125,869A
; CURRENT FILING DATE: 2002-11-19
; PRIOR FILING DATE: 60/284,534
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fc region binding polypeptide
US-10-125-869A-148

Query Match 20.8%; Score 40; DB 14; Length 23;
Best Local Similarity 43.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 YEYHPYGTLPVGPPE 16
Db 4 YWCNLMGVCPCANPPE 19

RESULT 6
US-10-462-262-372
; Sequence 372, Application US/10462262
; Publication No. US20040009534A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Dawson, Bruce M.
; TITLE OF INVENTION: PROTEIN ANALYSIS
; FILE REFERENCE: 10280-052001
; CURRENT APPLICATION NUMBER: US/10/462,262
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: US 60/388,642
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 430
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunoglobulin binding polypeptide
US-10-462-362-372

Query Match 20.8%; Score 40; DB 15; Length 23;
Best Local Similarity 43.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

Qy 1 YEVHPYGTLPVPGPE 16
Db 4 YWCLMGVCPANPGPE 19

RESULT 7
US-10-080-608A-71
; Sequence 71, Application US/10080608A
; Publication No. US20030198956A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/10/080,608A
; CURRENT FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 24
; TYPE: PRT
; ORGANISM: human immunodeficiency virus type 1
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 14
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-080-608A-71

Query Match 20.8%; Score 40; DB 14; Length 24;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 11 VGGPPEFKTLRVQNLGC 28
Db 9 IGPGRXFYTKNI--IGC 24

RESULT 8
US-10-371-067-2
; Sequence 2, Application US/10371067
; Publication No. US20040018587A1
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee

; APPLICANT: Williams, Mark K
; APPLICANT: Goldberg, Edward B
; TITLE OF INVENTION: Nanostructures containing antibody assembly subunits
; FILE REFERENCE: NANF.P-003
; CURRENT APPLICATION NUMBER: US/10/371,067
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/080,608
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 10/136,225
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 09/236,949
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: 08/542,003
; PRIOR FILING DATE: 1995-10-12
; PRIOR APPLICATION NUMBER: 08/322,760
; PRIOR FILING DATE: 1994-10-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 24
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: Fab59.complexed with a peptide mimic of the HIV-1 V3 loop
; OTHER INFORMATION: neutralization site.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-371-067-2

Query Match 20.8%; Score 40; DB 15; Length 24;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 8; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

Qy 11 VGGPPEFKTLRVQNLGC 28
Db 9 IGPGRXFYTKNI--IGC 24

RESULT 9
US-09-864-761-39770
; Sequence 39770, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 39770
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC005747.1
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.79
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
;; OTHER INFORMATION: EST_HUMAN HIT: H87835.1, EVALUE 2.00e-06
US-09-864-761-39770

Query Match 20.3%; Score 39; DB 9; Length 20;
Best Local Similarity 58.3%; Pred. No. 3.3e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 HPGYGLPVGCP 15
Db 1 HSWGTAKVGP 12

RESULT 10
US-09-864-761-46555
;; Sequence 46555, Application US/09864761
;; Patent No. US20020048763A1
;; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharron G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aecmica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 09/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664

;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 46555
;; LENGTH: 21
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC009973.2
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.9
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
;; OTHER INFORMATION: EST_HUMAN HIT: AL121516.1, EVALUE 8.00e-07
US-09-864-761-46555

Query Match 20.3%; Score 39; DB 9; Length 21;
Best Local Similarity 57.9%; Pred. No. 3.4e+02;
Matches 11; Conservative 1; Mismatches 3; Indels 4; Gaps 2;

Qy 2 EVHPYGLPVGPGPFKKT 20
Db 6 DVH-RGTL---PGPNHKT 20

RESULT 11
US-09-843-676-208
;; Sequence 208, Application US/09843676
;; Patent No. US20020164786A1
;; GENERAL INFORMATION:
;; APPLICANT: Cech, Thomas R.
;; Lingner, Joachim
;; Nakamura, Toru
;; Chapman, Karen B.
;; Morin, Gregg B.
;; Harley, Calvin
;; Andrews, William H.
;; TITLE OF INVENTION: No. US20020164786A1el Telomerase
;; NUMBER OF SEQUENCES: 225
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, 8th Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: United States of America
;; ZIP: 94111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/843,676
;; FILING DATE: 26-Apr-2001
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/854,050
;; FILING DATE: 09-MAY-1997
;; APPLICATION NUMBER: US/08/846,017
;; FILING DATE: 25-APR-1997
;; APPLICATION NUMBER: US/08/844,419
;; FILING DATE: 18-APR-1997
;; APPLICATION NUMBER: US/08/724,643
;; FILING DATE: 01-OCT-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002930US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 208:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-09-843-676-208

Query Match 20.3%; Score 39; DB 9; Length 23;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 HPGTLPVGP 15
Db 9 HPENLPQDP 20

RESULT 12
US-09-438-486-208
; Sequence 208, Application US/09438486
; Publication No. US20030009019A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030009019A1el Telomerase
; NUMBER OF SEQUENCES: 223
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,486
; FILING DATE: 12-NOV-1999
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/851,843
; FILING DATE: 06-MAY-1997
; CLASSIFICATION: 536

;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/846,017
;; FILING DATE: 25-APR-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/844,419
;; FILING DATE: 18-APR-1997
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/724,643
;; FILING DATE: 01-OCT-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Apple, Randolph T.
;; REGISTRATION NUMBER: 36,429
;; REFERENCE/DOCKET NUMBER: 015389-002931US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 208:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 23 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-09-438-486-208

Query Match 20.3%; Score 39; DB 10; Length 23;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 HPGTLPVGP 15
Db 9 HPENLPQDP 20

RESULT 13
US-10-053-758-208
; Sequence 208, Application US/10053758
; Publication No. US20030032075A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; APPLICANT: Lingner, Joachim
; APPLICANT: Nakamura, Toru
; APPLICANT: Chapman, Karen B.
; APPLICANT: Morin, Gregg B.
; APPLICANT: Harley, Calvin
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: NO. US20030032075A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/053,758
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US/08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US/08/846,017

;
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 23 amino acids
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-10-053-758-208

Query Match 20.3%; Score 39; DB 14; Length 23;
Best Local Similarity 58.3%; Pred.No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 HPYGTLPVGRGP 15
||| ||| |||
Db 9 HPRENLPQDPGP 20

RESULT 14
US-10-054-295-208
; Sequence 208, Application US/10054295
; Publication No. US20030044953A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030044953A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,295
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429

;
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 23 amino acids
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-10-054-295-208

Query Match 20.3%; Score 39; DB 14; Length 23;
Best Local Similarity 58.3%; Pred.No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 4 HPYGTLPVGRGP 15
||| ||| |||
Db 9 HPRENLPQDPGP 20

RESULT 15
US-10-054-611-208
; Sequence 208, Application US/10054611
; Publication No. US20030059787A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin
; Andrews, William H.
; TITLE OF INVENTION: No. US20030059787A1el Telomerase
; NUMBER OF SEQUENCES: 225
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/054,611
; FILING DATE: 18-Jan-2002
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/854,050
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002930US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid

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; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-10-054-611-208

Query Match      20.3%; Score 39; DB 14; Length 23;
Best Local Similarity 58.3%; Pred. No. 3.8e+02;
Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      4 HPYGTLPVGP GP 15
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Db      9 HPRENLPQDP GP 20

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Search completed: April 6, 2005, 13:57:33
Job time : 140 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 13:32:19 ; Search time 42 Seconds
(without alignments)
62.208 Million cell updates/sec

Title: US-09-647-544-2_COPY_952_986

Perfect score: 192

Sequence: 1 YEHVPYGLPVGPGPEFKTLRVQNLCGYVSGLI 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 250370

Minimum DB seq length: 0

Maximum DB seq length: 35

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

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- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	24.0	33	1	US-08-257-528B-84
2	46	24.0	33	1	US-08-460-602A-84
3	46	24.0	33	1	US-08-463-966A-84
4	46	24.0	33	1	US-08-465-217A-84
5	46	24.0	33	2	US-08-464-329A-84
6	46	24.0	33	2	US-08-462-507A-84
7	46	24.0	33	2	US-08-467-881A-84
8	46	24.0	34	3	US-09-141-833-11
9	45.5	23.7	33	1	US-08-257-528B-83
10	45.5	23.7	33	1	US-08-460-602A-83
11	45.5	23.7	33	1	US-08-463-966A-83
12	45.5	23.7	33	1	US-08-465-217A-83
13	45.5	23.7	33	2	US-08-464-329A-83
14	45.5	23.7	33	2	US-08-462-507A-83
15	45.5	23.7	33	2	US-08-467-881A-83
16	45	23.4	35	3	US-08-513-968-13
17	43.5	22.7	33	1	US-08-257-528B-81
18	43.5	22.7	33	1	US-08-460-602A-81
19	43.5	22.7	33	1	US-08-463-966A-81
20	43.5	22.7	33	1	US-08-465-217A-81
21	43.5	22.7	33	2	US-08-464-329A-81
22	43.5	22.7	33	2	US-08-462-507A-81
23	43.5	22.7	33	2	US-08-467-881A-81
24	43	22.4	18	1	US-08-257-528B-50
25	43	22.4	18	1	US-08-460-602A-50
26	43	22.4	18	1	US-08-463-966A-50
27	43	22.4	18	1	US-08-465-217A-50

28	43	22.4	18	2	US-08-464-329A-50	Sequence 50, Appl
29	43	22.4	18	2	US-08-462-507A-50	Sequence 50, Appl
30	43	22.4	18	2	US-08-467-881A-50	Sequence 50, Appl
31	43	22.4	23	3	US-08-513-968-71	Sequence 71, Appl
32	43	22.4	23	3	US-08-513-968-72	Sequence 72, Appl
33	43	22.4	33	1	US-08-257-528B-41	Sequence 41, Appl
34	43	22.4	33	1	US-08-257-528B-80	Sequence 80, Appl
35	43	22.4	33	1	US-08-460-602A-41	Sequence 41, Appl
36	43	22.4	33	1	US-08-460-602A-80	Sequence 80, Appl
37	43	22.4	33	1	US-08-463-966A-41	Sequence 41, Appl
38	43	22.4	33	1	US-08-463-966A-80	Sequence 80, Appl
39	43	22.4	33	1	US-08-465-217A-41	Sequence 41, Appl
40	43	22.4	33	1	US-08-465-217A-80	Sequence 80, Appl
41	43	22.4	33	2	US-08-464-329A-41	Sequence 41, Appl
42	43	22.4	33	2	US-08-464-329A-80	Sequence 80, Appl
43	43	22.4	33	2	US-08-462-507A-41	Sequence 41, Appl
44	43	22.4	33	2	US-08-462-507A-80	Sequence 80, Appl
45	43	22.4	33	2	US-08-467-881A-41	Sequence 41, Appl

ALIGNMENTS

RESULT 1
US-08-257-528B-84
; Sequence 84, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Random Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-257-528B-84

Query Match 24.0%; Score 46; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 8.7;
Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;
Qy 8 TLPVGPGEFKTT-----LRVQNLG 27
Db 5 SIPIGPGRAFTTGYKYKWKIEPLG 30

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RESULT 2
US-08-460-602A-84
; Sequence 84, Application US/08460602A
; Patent No. 5795955
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,602A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 84:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-460-602A-84

Query Match 24.0%; Score 46; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 8.7;
Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;

Qy 8 TLPVGPPEPKTT-----LRVQNLG 27
Db 5 SIPIGPGRAFYTTGYKYKVKVIEPLG 30

RESULT 3
US-08-463-966A-84
; Sequence 84, Application US/08463966A
; Patent No. 5795955
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
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; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,966A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 84:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-463-966A-84

Query Match 24.0%; Score 46; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 8.7;
Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;

Qy 8 TLPVGPPEPKTT-----LRVQNLG 27
Db 5 SIPIGPGRAFYTTGYKYKVKVIEPLG 30

RESULT 4
US-08-465-217A-84
; Sequence 84, Application US/08465217A
; Patent No. 5800822
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,217A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
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; Sequence 84, Application US/08467881A
; Patent No. 5951986
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08467,881A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-488 MIS:jbb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-467-881A-84

Query Match 24.0%; Score 46; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 8.7;
Matches 9; Conservative 7; Mismatches 4; Indels 6; Gaps 1;

Qy 8 TLPVGGPPEFKTT-----LRVQNLG 27
Db 5 SIPIGPGRAFTYTGYYKVKVIEPLG 30

RESULT 8
US-09-141-833-11
; Sequence 11, Application US/09141833
; Patent No. 6168784
; GENERAL INFORMATION:
; APPLICANT: OFFORD, ROBIN E
; APPLICANT: THOMPSON, DARREN
; APPLICANT: WILKEN, JILL
; TITLE OF INVENTION: N-TERMINAL MODIFICATIONS OF RANTES AND METHODS OF USE
; FILE REFERENCE: GRFN-026/0305
; CURRENT APPLICATION NUMBER: US/09141,833
; CURRENT FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: 60/056,292
; EARLIER FILING DATE: 1997-09-03
; EARLIER APPLICATION NUMBER: 60/077,874
; EARLIER FILING DATE: 1998-03-13
; EARLIER APPLICATION NUMBER: 60/090,834

; EARLIER FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-141-833-11

Query Match 24.0%; Score 46; DB 3; Length 34;
Best Local Similarity 47.4%; Pred. No. 9;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 8 TLPVGGPPEFKTTLRVQNL 26
Db 11 SISIGPGRAFTTQIVGNL 29

RESULT 9
US-08-257-528B-83
; Sequence 83, Application US/08257528B
; Patent No. 5639854
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08257,528B
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-336 MIS:jbb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-257-528B-83

Query Match 23.7%; Score 45.5; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLPVGGPPEFKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 10
US-08-460-602A-83
; Sequence 83, Application US/08460602A
; Patent No. 5759769
; GENERAL INFORMATION:

APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,602A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 83:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-602A-83

Query Match 23.7%; Score 45.5; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPGPGPEFKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 11
US-08-463-966A-83
Sequence 83, Application US/08463966A
Patent No. 5795955
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,966A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 83:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-83

Query Match 23.7%; Score 45.5; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy 2 EVHPYG-----TLVPGPGPEFKTT 20
Db 7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 12
US-08-465-217A-83
Sequence 83, Application US/08465217A
Patent No. 5800822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 83:
LENGTH: 33 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-463-966A-83

```
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-465-217A-83

Query Match      23.7%; Score 45.5; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy  2 EVHPYG-----TLPVGPGEPEKTT 20
Db  7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 13
US-08-464-329A-83
; Sequence 83, Application US/08464329A
; Patent No. 5817754
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,329A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-449 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-464-329A-83

Query Match      23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;
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; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-465-217A-83

Query Match      23.7%; Score 45.5; DB 1; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy  2 EVHPYG-----TLPVGPGEPEKTT 20
Db  7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 14
US-08-462-507A-83
; Sequence 83, Application US/08462507A
; Patent No. 5876731
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,507A
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-451 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-462-507A-83

Query Match      23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

Qy  2 EVHPYG-----TLPVGPGEPEKTT 20
Db  7 KIEPLGVAPNTRKSIPIGPGRAFYTT 32

RESULT 15
US-08-467-881A-83
; Sequence 83, Application US/08467881A
; Patent No. 5951986
; GENERAL INFORMATION:
; APPLICANT: SIA, Charles D.Y.
; APPLICANT: CHONG, Pele
```

```

; APPLICANT: KLEIN, Michel H.
; TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
; NUMBER OF SEQUENCES: 101
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,881A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,528
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,378
; FILING DATE: 09-JUN-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, MICHAEL I.
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-488 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 83:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-467-881A-83

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Query Match      23.7%; Score 45.5; DB 2; Length 33;
Best Local Similarity 34.6%; Pred. No. 10;
Matches 9; Conservative 5; Mismatches 5; Indels 7; Gaps 1;

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Qy      2 EVHPVG-----TLPVGPGEFKTT 20
         ::|||:::|||
Db      7 KIEPLGVAPNTRKSIPIGGRFYTT 32

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Search completed: April 6, 2005, 13:45:31
Job time : 43 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:42:11 ; Search time 43 Seconds
(without alignments)
49.227 Million cell updates/sec

Title: US-09-647-544-7

Perfect score: 114

Sequence: 1 KLGFPAHKKIPBEKREKLEQ 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4267

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	35.1	19	2 A49725	valine-tRNA ligase
2	30	26.3	20	2 I53671	neurofilament heavy
3	29	25.4	17	2 S10786	enamelin, 26K - bo
4	29	25.4	20	2 S43627	cytochrome-c oxida
5	28	24.6	10	2 S65385	cytochrome-c oxida
6	27	23.7	8	2 I64832	Ca2+-transporting
7	27	23.7	15	2 PA0041	plastoquinol-plast
8	27	23.7	16	2 S13898	alkaline phosphata
9	27	23.7	17	2 G83975	hypothetical prote
10	27	23.7	18	2 A81220	epiloin receptor m
11	27	23.7	20	2 S11416	ribosomal protein
12	26	22.8	15	2 S36891	ribosomal protein
13	26	22.8	18	2 E33178	78K heat shock pro
14	26	22.8	21	2 PC7043	ubiquitin carboxyl
15	26	22.8	22	2 F33084	ribosomal protein
16	26	22.8	22	2 PC4388	sulfite reductase
17	25	21.9	16	2 JH0517	insulin-like growt
18	25	21.9	16	2 A35552	caldesmon - turkey
19	25	21.9	18	2 S39845	2-aminobenzoate-Co
20	25	21.9	20	2 D49164	chromogranin-B - r
21	25	21.9	20	2 S06149	photosystem I chai
22	25	21.9	20	2 S77983	cytochrome-c oxida
23	25	21.9	22	2 PX0078	alanine dehydrogen
24	24.5	21.5	21	2 S00189	motilin - dog (ten
25	24	21.1	14	2 S65392	cytochrome-c oxida
26	24	21.1	18	2 B44995	alkanal monooxygen
27	24	21.1	19	2 A37968	neural surface pro
28	24	21.1	22	2 H86433	protein TI7H7.9 [i
29	23.5	20.6	19	2 S02808	nucleolin - bovine

30	23	20.2	14	2 A49018	myosin heavy chain
31	23	20.2	15	2 C37765	hypothetical prote
32	23	20.2	18	2 I40062	shikimate 5-dehydr
33	23	20.2	19	2 S69166	ferredoxin b - Jap
34	23	20.2	20	2 JP0070	ribosomal protein
35	23	20.2	20	2 A31516	lectin, galactose/
36	23	20.2	20	2 S06150	photosystem I chai
37	23	20.2	20	2 S19618	globin - polychaet
38	23	20.2	21	2 S78416	ribosomal protein
39	23	20.2	22	2 JP0071	ribosomal protein
40	23	20.2	22	2 C64330	ribosomal protein
41	23	20.2	22	2 S78007	fucosyltransferase
42	23	20.2	22	2 S48196	fucosyltransferase
43	22.5	19.7	20	2 A05310	apolipoprotein B -
44	22	19.3	10	2 S43625	cytochrome-c oxida
45	22	19.3	12	2 S16335	beta-conglycinin a

ALIGNMENTS

RESULT 1

A49725 valine-tRNA ligase (EC 6.1.1.9) - rabbit (fragment)

N;Alternate names: valyl-tRNA synthetase

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Jun-2002

C;Accession: A49725

R;Bec, G.; Kerjan, P.; Waller, J.P.

J. Biol. Chem. 269, 2086-2092, 1994

A;Title: Reconstitution in Vitro of the valyl-tRNA synthetase-elongation factor (EF) 1be

Ita subunit in complex formation.

A;Reference number: A49725; MUID:94124563; PMID:8294461

A;Accession: A49725

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-19 <BEC>

C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 35.1%; Score 40; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 30;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Oy 9 KIPEEKREKLEQ 22

Db 2 QLPXEAKKNEKLEK 15

RESULT 2

I53671 neurofilament heavy subunit - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004

C;Accession: I53671

R;Figlewicz, D.A.; Rouleau, G.A.; Krizus, A.; Julien, J.P.

Gene 132, 297-300, 1993

A;Title: Polymorphism in the multi-phosphorylation domain of the human neurofilament hea

A;Reference number: I53671; MUID:94040777; PMID:8224877

A;Accession: I53671

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-20 <RES>

A;Cross-references: UNIPROT:Q16070; GB:S66488; NID:g452861; PIDN:AAB28609.1; PID:g452862

C;Genetics:

A;Gene: GDB:NEFH

A;Cross-references: GDB:120225; OMIM:162230

A;Map position: 22q12.1-22q13.1

Query Match 26.3%; Score 30; DB 2; Length 20;

Best Local Similarity 53.8%; Pred. No. 7.1e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Oy 9 KIPEEKREKLE 21

```
Db      |||: |||
        6 KSPEKAKSPKEE 18

RESULT 3
SI0786
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Mar-1997 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
C:Accession: SI0786
R:Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A:Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelin' is albumin
A:Reference number: SI0780; MUID:90336641; PMID:2379503
A:Accession: SI0786
A:Molecule type: protein
A:Residues: 1-17 <STR>
A:Cross-references: UNIPROT:Q7M2M6
C:Keywords: enamel; phosphoprotein

Query Match      25.4%; Score 29; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 HKKIP 11
        |||||
        10 HKKIP 14

RESULT 4
S43627
cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)
C:Species: Salmo gairdneri (trout)
C:Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 02-Jul-1998
C:Accession: S43627
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIa of cytochrome c oxidase
A:Reference number: S43624; MUID:94237150; PMID:8181469
A:Accession: S43627
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <FRE>
C:Keywords: electron transfer; membrane-associated complex; oxidoreductase; respiratory

Query Match      25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.7e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy      8 KKIPPEEKREKLEQ 22
        |||: |||
        4 KGIPDSEQATGLSE 18

RESULT 5
S65385
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 07-May-1999
C:Accession: S65385
R:Schaegger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequence
A:Reference number: S65372; MUID:93324529; PMID:7601105
A:Accession: S65385
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SCH>
C:Keywords: oxidoreductase

Query Match      24.6%; Score 28; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      9 KIPEEEK 15
        |||: |||
        4 KVPEKQK 10
```

```
RESULT 6
I64832
Ca2+-transporting ATPase (EC 3.6.3.8) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C:Accession: I64832
R:Wu, K.
Am. J. Physiol. 264, 333-341, 1993
A:Title: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase in rat
A:Reference number: I51892
A:Accession: I64832
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-8 <RES>
A:Cross-references: UNIPROT:Q63139; GB:M99223; NID:g203644; PIDN:AAA40992.1; PID:g203646
C:Genetics:
A:Gene: SERCALB
C:Keywords: hydrolase
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```
Query Match      23.7%; Score 27; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      11 PEEKRE 17
        |||: |||
        2 PEDERRK 8
```

```
RESULT 7
PA0041
plastoquinol-plastocyanin reductase (EC 1.10.99.1) - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: PA0041
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
A:Reference number: PA0001
A:Accession: PA0041
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Cross-references: UNIPROT:Q92R03; UNIPROT:Q94E14; UNIPROT:Q9FYB6
A:Experimental source: leaf
C:Keywords: oxidoreductase
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Query Match      23.7%; Score 27; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      9 KIPEEKR 16
        |||: |||
        8 RVFDMERK 15
```

```
RESULT 8
SI3898
alkaline phosphatase (EC 3.1.3.1) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: SI3898
R:Fujimori-Arai, Y.; Koyama, I.; Hirano, K.; Sakagishi, Y.; Komoda, T.
Arch. Biochem. Biophys. 284, 320-325, 1991
A:Title: Purification and partial characterization of intestinal-like alkaline phosphatase from rabbit
A:Reference number: SI3898; MUID:91112827; PMID:1989515
A:Accession: SI3898
A:Status: preliminary
A:Molecule type: protein
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A;Residues: 1-16 <FU>
A;Cross-references: UNIPROT:Q7M2K8
C;Keywords: phosphoric monoester hydrolase

Query Match 23.7%; Score 27; DB 2; Length 16;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 IPEEEK 15
| | | | |
Db 2 IPEEEE 7

RESULT 9

G83975
Hypothetical protein BH2607 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83975
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83975
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-17 <STO>
A;Cross-references: UNIPROT:Q9K9N8; GB:AP001516; GB:BA000004; NID:G10175192; PIDN:BA063
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2607

Query Match 23.7%; Score 27; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 7; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 8 KKIPEEEKREEKLE 21
| | | | |
Db 2 KEIPTKMKTEKDE 15

RESULT 10

A61220
epsilon receptor modulating protein (EC 3.4.21.-) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A61220
R;Matsushita, S.; Katz, D.H.
Cell. Immunol. 137, 252-259, 1991
A;Title: The murine epsilon receptor modulating protein: a novel serine protease which m
A;Reference number: A61220; MUID:91356570; PMID:1679381
A;Accession: A61220
A;Molecule type: protein
A;Residues: 1-18 <WAR>
A;Cross-references: UNIPROT:Q7M060
C;Comment: This serine proteinase from a T cell hybridoma does not reduce levels of CD23
C;Keywords: hydrolase; serine proteinase

Query Match 23.7%; Score 27; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 8 KKIPEEEKREEK 19
| | | | |
Db 2 KPAPKKEKKK 13

RESULT 11

S11416
ribosomal protein L6, cytosolic [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jul-2000
C;Accession: S11416

R;Wittmann-Liebold, B.; Geissler, A.W.; Lin, A.; Wool, I.G.
J. Supramol. Struct. 12, 425-433, 1979
A;Title: Sequence of the amino-terminal region of rat liver ribosomal proteins S4, S6, S8
A;Reference number: S11413; MUID:80252792; PMID:398910
A;Accession: S11416

A;Molecule type: protein
A;Residues: 1-20 <WIT>
A;Note: the protein is designated as ribosomal protein L6
C;Keywords: protein biosynthesis; ribosome

Query Match 23.7%; Score 27; DB 2; Length 20;
Best Local Similarity 35.7%; Pred. No. 1.8e+03;
Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 6 AHKKIPEEEKREEK 19
| | | | |
Db 1 AGEKAEKPKKKEQK 14

RESULT 12

S36891
ribosomal protein - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S36891
R;Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A;Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac.
A;Reference number: S36887; MUID:94009653; PMID:8405418
A;Accession: S36891
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <OHA>
A;Cross-references: UNIPROT:Q9R545

Query Match 22.8%; Score 26; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 8 KKIPEEEKREEK 19
| | | | |
Db 3 KNVPANSRRKAK 14

RESULT 13

E33178
78K heat shock protein - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 23-Mar-1993
C;Accession: E33178
R;Ward, L.D.; Hong, J.; Whitehead, R.H.; Simpson, R.J.
Electrophoresis 11, 883-891, 1990
A;Title: Development of a database of amino acid sequences for human colon carcinoma pro.
A;Reference number: A33178; MUID:91176935; PMID:2079031
A;Accession: E33178
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-18 <WAR>

Query Match 22.8%; Score 26; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 12 EEEKREE 18
| | | | |
Db 2 EEDKKED 8

RESULT 14

PC7043
ubiquitin carboxyl-terminal hydrolase (EC 3.1.1.-) homolog - yeast (Pichia anomala) (fra
N;Alternate names: ALX1 protein
C;Species: Pichia anomala, Candida pelliculosa

C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 09-Jul-2004
 C;Accession: PC7043
 R/Sakajo, S.; Minagawa, N.; Yoshimoto, A.
 Biosci. Biotechnol. Biochem. 63, 1889-1894, 1999
 A;Title: Structure and regulatory expression of a single copy alternative oxidase gene
 A;Reference number: JC7145; MUID:20101471; PMID:10635554
 A;Accession: PC7043
 A;Molecule type: DNA
 A;Residues: 1-21 <SAK>
 A;Cross-references: UNIPROT:Q9P987; DDBJ:AB026726
 C;Genetics:
 A;Gene: aix1
 C;Keywords: hydrolase

Query Match 22.8%; Score 26; DB 2; Length 21;
 Best Local Similarity 50.0%; Pred. No. 2.7e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 13 EKREKXLEQ 22
 | : | | : | :
 Db 12 EDKREGKEE 21

RESULT 15
 F33084
 ribosomal protein L18 - Haloferax mediterranei (fragment)
 N;Alternate names: ribosomal protein HL13
 C;Species: Haloferax mediterranei
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: F33084
 R;McDougall, J.
 submitted to the Protein Sequence Database, June 1990
 A;Reference number: A33084
 A;Accession: F33084
 A;Molecule type: Protein
 A;Residues: 1-22 <MCD>
 A;Cross-references: UNIPROT:P50561
 A;Experimental source: strain DSM 1411
 C;Superfamily: rat ribosomal protein L5
 C;Keywords: protein biosynthesis; ribosome

Query Match 22.8%; Score 26; DB 2; Length 22;
 Best Local Similarity 30.8%; Pred. No. 2.7e+03;
 Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 9 KIEEEKKEKLE 21
 | : | : | : | :
 Db 7 KVPMMRRREVTD 19

Search completed: April 6, 2005, 14:59:35
 Job time : 45 secs


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RX MEDLINE=92319557; PubMed=1352398;
RA Hogg A., Onadim Z., Baird P.N., Cowell J.K.;
RT "Detection of heterozygous mutations in the RB1 gene in retinoblastoma
RT patients using single-strand conformation polymorphism analysis and
RT polymerae chain reaction sequencing.";
RL Oncogene 7:1445-1451(1992).
DR EMBL; AY243567; AAC62758.1; -.
DR EMBL; L41913; AAA65748.1; -.
FT NON TER 1 1
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1871 MW; 3A6A9791FD68E1E9 CRC64;

Query Match 28.1%; Score 32; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 8 KKIPEEKREKLEQ 22
Db 1 KHLFGESKFOQKLA 15

RESULT 3
Q91983 PRELIMINARY; PRT; 19 AA.
AC Q91983;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MHC (19 AA) (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA McCarthy J.G.; Heywood S.M.;
RL Submitted (FEB-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; X06251; CAA29593.1; -.
DR PIR; S39082; S39082.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2387 MW; 2DD5C6816CD4D6EC CRC64;

Query Match 27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 70.0%; Pred. No. 2.8e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 FAHKKIPEEE 14
Db 10 FHSKKIEEEE 19

RESULT 4
Q789B3 PRELIMINARY; PRT; 19 AA.
AC Q789B3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Myosin heavy chain (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;

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RN [1]
RP SEQUENCE FROM N.A.
RA Lagrutta A.A., McCarthy J.G., Scherzinger C.A., Heywood S.M.;
RT "Identification and developmental expression of a novel embryonic
RT myosin heavy-chain gene in chicken.";
RL DNA 8:39-50(1989).
DR EMBL; M24691; AAA48950.1; -.
FT NON TER 1 1
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2387 MW; 2DD5C6816CD4D6EC CRC64;

Query Match 27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 70.0%; Pred. No. 2.8e+03;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 FAHKKIPEEE 14
Db 10 FHSKKIEEEE 19

RESULT 5
Q9380 PRELIMINARY; PRT; 13 AA.
AC Q9380;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IFA binding protein (sp10) (Fragment).
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Eurosid II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Dok; TISSUE=Curd surface;
RA Wallis G.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97678; CAA66268.1; -.
FT NON TER 1 1
SQ SEQUENCE 13 AA; 1413 MW; DID4EA3926B42772 CRC64;

Query Match 26.3%; Score 30; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.6e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 AHKKIPEEE 13
Db 2 AEKKVPKE 9

RESULT 6
Q16070 PRELIMINARY; PRT; 20 AA.
AC Q16070;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Neurofilament heavy subunit (Fragment).
GN Name=NEFH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94040777; PubMed=8224877; DOI=10.1016/0378-1119(93)90211-K;
RA Figlewicz D.A., Rouleau G.A., Krizus A., Julien J.P.;
RT "Polymorphism in the multi-phosphorylation domain of the human
RT neurofilament heavy-subunit-encoding gene.";
RL Gene 132:297-300(1993).
DR EMBL; S66488; AAB28609.1; -.
DR PIR; I53671; I53671.

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FT  NON TER      20      20
SQ  SEQUENCE 20 AA; 2198 MW;  E9A0975B41FD8082 CRC64;

Query Match      26.3%; Score 30; DB 2; Length 20;
Best Local Similarity 53.8%; Pred. No. 4.1e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy  9 KIPEEKKEEKL 21
Db  6 KSPKAKSPKEEE 18

RESULT 7
Q9RSU3
ID  Q9RSU3 PRELIMINARY; PRT; 22 AA.
AC  Q9RSU3;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  2-amino-benzoate-CoA LIGASE=E2 (Fragment).
OS  Pseudomonas.
OC  Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC  Pseudomonadaceae.
OX  NCBI_TaxID=286;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=91358327; PubMed=1885526;
RA  Alteschmidt U., Oswald B., Fuchs G.;
RT  "Purification and characterization of benzoate-coenzyme A ligase and
RT  2-aminobenzoate-coenzyme A ligases from a denitrifying Pseudomonas
RT  sp.";
RL  J. Bacteriol. 173:5494-5501(1991).
FT  NON TER      1
FT  NON TER      22
SQ  SEQUENCE 22 AA; 2526 MW;  5D37FA76363F8792 CRC64;

Query Match      26.3%; Score 30; DB 2; Length 22;
Best Local Similarity 37.5%; Pred. No. 4.5e+03;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy  5 FAHKKIPPEEKREKL 20
Db  7 FARDXPTEQTESL 22

RESULT 8
Q9TRY7
ID  Q9TRY7 PRELIMINARY; PRT; 20 AA.
AC  Q9TRY7;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Insulin-like growth factor-binding protein-5, IGFBP-5 (Fragment).
OS  Sus sp.
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9826;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=92049376; PubMed=1719383;
RA  Shimasaki S., Gao L., Shimonaka M., Ling N.;
RT  "Isolation and molecular cloning of insulin-like growth factor-binding
RT  protein-6.";
RL  Mol. Endocrinol. 5:938-948(1991).
FT  NON TER      1
FT  NON TER      20
SQ  SEQUENCE 20 AA; 2185 MW;  F77C348AFA94EF9 CRC64;

Query Match      25.9%; Score 29.5; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 7; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

Qy  2 LGFFAHKKIPPEEK 15

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Db  1 LGSFVHXE-PADEX 13

RESULT 9
Q7M2M6
ID  Q7M2M6 PRELIMINARY; PRT; 17 AA.
AC  Q7M2M6;
DT  01-MAR-2004 (TrEMBLrel. 26, Created)
DT  01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  Enamelin, 26K (Fragment).
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC  Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=90336641; PubMed=2379503;
RA  Strawich E., Glimcher M.J.;
RT  "Tooth 'enamelins' identified mainly as serum proteins. Major
RT  'enamelin' is albumin.";
RL  Eur. J. Biochem. 191:47-56(1990).
DR  PIR; S10786; S10786.
FT  NON TER      1
FT  NON TER      17
SQ  SEQUENCE 17 AA; 2137 MW;  FFA54E4CEE066720 CRC64;

Query Match      25.4%; Score 29; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  7 HKKIP 11
Db  10 HKKIP 14

RESULT 10
COXF ONCMY
ID  COXF ONCMY STANDARD; PRT; 20 AA.
AC  P80329;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Cytochrome c oxidase polypeptide Vb-heart (EC 1.9.3.1) (Fragment).
OS  Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC  Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX  NCBI_TaxID=8022;
RN  [1]
RP  SEQUENCE.
RX  TISSUE=Heart;
RX  MEDLINE=94237150; PubMed=8181469;
RA  Freund R., Kadenbach B.;
RT  "Identification of tissue-specific isoforms for subunits Vb and Vifa
RT  of cytochrome c oxidase isolated from rainbow trout.";
RL  Eur. J. Biochem. 221:1111-1116(1994).
CC  -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
CC  chains of cytochrome c oxidase, the terminal oxidase in
CC  mitochondrial electron transport.
CC  -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC  c + 2 H(2)O.
CC  -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC  -!- SIMILARITY: Belongs to the cytochrome c oxidase Vb family.
DR  InterPro; IPR002124; COX5B.
DR  PROSITE; PS00848; COX5B; PARTIAL.
KW  Direct protein sequencing; Inner membrane; Mitochondrion;
FT  NON TER      20
FT  NON TER      20
SQ  SEQUENCE 20 AA; 2184 MW;  6A8E00CB33E92BD7 CRC64;

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Q6LDS7
ID Q6LDS7 PRELIMINARY; PRT; 9 AA.
AC Q6LDS7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ca2+ ATPase (Fragment);
DS Oryctolagus cuniculus (Rabbit).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fast twitch muscle;
RX MEDLINE=89169602; PubMed=2965149;
RA Korczak B., Zarain-Herzberg A., Brandl C.J., Ingles C.J., Green N.M.,
RA MacLennan D.H.;
RT "Structure of the rabbit fast-twitch skeletal muscle Ca2+-ATPase
gene";
RL J. Biol. Chem. 263:4813-4819(1988).
DR EMBL; M20532; AAA31174.1; -.
FT NON TER 1
SQ SEQUENCE 9 AA; 1173 MW; 8235140B1AAB076A CRC64;

Query Match 23.7%; Score 27; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 11 PEEKRE 17
Db 3 PEDERRK 9

Search completed: April 6, 2005, 14:55:45
Job time : 176 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 14:41:35 ; Search time 174 Seconds
(without alignments)
48.901 Million cell updates/sec

Title: US-09-647-544-7
Perfect score: 114
Sequence: 1 KLGFPAHKIPEREKLEQ 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 740715

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	22	3	AA32244 Human int
2	44	38.6	19	6	ABP56388 Polyamion
3	44	38.6	20	4	AA59156 Alpha IIB
4	43	37.7	20	2	AA88078 Integrin
5	43	37.7	20	4	AA59147 Alpha IIB
6	42	36.8	19	2	AAW48683 Amino aci
7	39	34.2	7	8	ADA27160 Human int
8	39	34.2	7	8	ADI39445 Integrin
9	39	34.2	15	6	ABP94377 HLA prote
10	39	34.2	15	6	ABP93904 HLA prote
11	39	34.2	15	6	ABP94921 HLA prote
12	39	34.2	15	6	ABP95230 HLA prote
13	39	34.2	20	5	AAU85587 Lung tumo
14	39	34.2	20	6	ABU69559 Human lun
15	39	34.2	20	6	ABU66462 Lung canc
16	39	34.2	20	7	ADH47374 Human lun
17	39	34.2	20	8	ADJ21293 Human lun
18	38	33.3	22	4	AA16576 Peptide #
19	38	33.3	22	4	AB20986 Protein #
20	38	33.3	22	4	AA68751 Human bon
21	37	32.5	15	6	ABP95115 HLA prote
22	37	32.5	15	6	ABP94987 HLA prote
23	37	32.5	15	6	ABP93956 HLA prote
24	37	32.5	15	6	ABP93368 HLA prote
25	37	32.5	15	6	ABP94457 HLA prote

26	37	32.5	15	6	ABP95241	Abp95241 HLA prote
27	37	32.5	15	6	ABP94244	Abp94244 HLA prote
28	37	32.5	15	6	ABP94458	Abp94458 HLA prote
29	37	32.5	15	6	ABP93790	Abp93790 HLA prote
30	37	32.5	15	6	ABP94825	Abp94825 HLA prote
31	37	32.5	15	8	ADI32231	Adi32231 Cosmetic
32	37	32.5	15	8	ADO76553	Ado76553 Human 213
33	37	32.5	20	5	AAU85588	AAU85588 Lung tumo
34	37	32.5	20	6	ABU69560	Abu69560 Human lun
35	37	32.5	20	6	ABU66463	Abu66463 Lung canc
36	37	32.5	20	7	ADH47375	Adh47375 Human lun
37	37	32.5	20	8	ADJ21294	Adj21294 Human lun
38	36	31.6	13	4	AA899530	Aab899530 Human Hsp
39	36	31.6	13	5	ABB74746	Abb74746 Transcrip
40	36	31.6	14	4	AA59149	Aab59149 Alpha IIB
41	36	31.6	16	4	AA899524	Aab899524 Human Hsp
42	36	31.6	16	4	AA59148	Aab59148 Alpha IIB
43	36	31.6	17	4	AA899533	Aab899533 Hsp70B' i
44	36	31.6	18	3	AAV52610	AAV52610 v-myb enc
45	36	31.6	19	2	AAW14811	AAW14811 myb onco

ALIGNMENTS

RESULT 1

AA32244
ID AA32244 standard; peptide; 22 AA.

XX AC AA32244;

XX DT 15-FEB-2000 (first entry)

XX DE Human integrin subunit alpha-10 cytoplasmic domain peptide.
XX KW Integrin alpha-10; ISa10; human; trauma; rheumatoid arthritis;
XX KW osteoarthritis; osteoarthritis; cancer; atherosclerosis; inflammation;
XX KW therapy; cartilage; chondrocyte; osteoblast; fibroblast; vaccine; marker.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	22	3	AA32244 Human int
2	44	38.6	19	6	ABP56388 Polyamion
3	44	38.6	20	4	AA59156 Alpha IIB
4	43	37.7	20	2	AA88078 Integrin
5	43	37.7	20	4	AA59147 Alpha IIB
6	42	36.8	19	2	AAW48683 Amino aci
7	39	34.2	7	8	ADA27160 Human int
8	39	34.2	7	8	ADI39445 Integrin
9	39	34.2	15	6	ABP94377 HLA prote
10	39	34.2	15	6	ABP93904 HLA prote
11	39	34.2	15	6	ABP94921 HLA prote
12	39	34.2	15	6	ABP95230 HLA prote
13	39	34.2	20	5	AAU85587 Lung tumo
14	39	34.2	20	6	ABU69559 Human lun
15	39	34.2	20	6	ABU66462 Lung canc
16	39	34.2	20	7	ADH47374 Human lun
17	39	34.2	20	8	ADJ21293 Human lun
18	38	33.3	22	4	AA16576 Peptide #
19	38	33.3	22	4	AB20986 Protein #
20	38	33.3	22	4	AA68751 Human bon
21	37	32.5	15	6	ABP95115 HLA prote
22	37	32.5	15	6	ABP94987 HLA prote
23	37	32.5	15	6	ABP93956 HLA prote
24	37	32.5	15	6	ABP93368 HLA prote
25	37	32.5	15	6	ABP94457 HLA prote

Claim 21; Page 53; 90pp; English.

This sequence represents a fragment of novel human chondrocyte integrin subunit alpha-10 (ISa10, see AA32242), corresponding to the C-terminal cytoplasmic domain of the protein. The invention relates to a recombinant or isolated integrin heterodimer comprising the alpha10 subunit in association with subunit beta (especially beta-1). The integrin heterodimer, or the subunit alpha-10, or a fragment of it such as the present sequence, can be used as a marker or target of all types of cells, e.g. of chondrocytes, osteoblasts and fibroblasts. They can also be used: for treating pathological conditions involving ISa10, such as damage to cartilage, trauma, rheumatoid arthritis or osteoarthritis; for

CC detecting the formation of cartilage during embryonal development,
 CC physiological or therapeutic repair of cartilage, or detecting
 CC regeneration of cartilage or chondrocytes during transplantation of
 CC cartilage or chondrocytes; for selection and analysis or for sorting,
 CC isolating or purification of chondrocytes and for in vitro studies of
 CC differentiation of chondrocytes; and as a target for anti-adhesive drugs
 CC or molecules in tendon, ligament, skeletal muscle or other tissues where
 CC adhesion impairs the function of the tissue (all claimed). ISa10 binding
 CC entities can be used to determine the differentiation-state of cells
 CC during embryonic development, angiogenesis or development of cancer, in
 CC pathological conditions such as rheumatoid arthritis, osteoarthritis or
 CC cancer, in tissue regeneration or in therapeutic and physiological
 CC repair of cartilage (claimed). A vaccine comprising the integrin
 CC heterodimer or subunit alpha-10 is also claimed. ISa10 polynucleotides,
 CC vectors, host cells and methods of producing recombinant ISa10 are also
 CC claimed

XX Sequence 22 AA;

Query Match 100.0%; Score 114; DB 3; Length 22;
 Best Local Similarity 100.0%; Pred. No. 5.7e-09;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLGFFAHKKIPBEKREKLEQ 22
 |||||
 Db 1 KLGFFAHKKIPBEKREKLEQ 22

RESULT 2

ABP56388
 ID ABP56388 standard; peptide; 19 AA.

XX

AC ABP56388;

XX 11-MAR-2003 (first entry)

XX Polyanionic polymer related peptide #3.

XX Polyanionic polymer; bioactivity; water solubility.

XX Synthetic.

XX WO200277036-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US008614.

XX 21-MAR-2001; 2001US-027705P.

XX (LEUN/) LEUNG D W.

XX Leung DW, Bergman PA, Lofquist A, Pietz GE, Tompkins CK;

XX Waggoner DW;

XX WPI; 2003-058367/05.

XX Producing monodispersed preparation of polyanionic polymer for therapy,
 PT by expressing vector comprising ligation product of oligonucleotides
 PT encoding glutamate/aspartate residues in host cell and isolating the
 PT product.
 XX Example 1; Fig 2; 74pp; English.
 XX The present invention describes a method (M) for producing a
 CC monodispersed preparation of a polyanionic polymer (PP) larger than 10
 CC kD. (M) involves inserting into an expression vector (EV) a ligation
 CC product formed by ligating together oligonucleotides that encode
 CC glutamate/aspartate residues, expressing EV in a host cell, and isolating
 CC the protein product (P) of EV, where (P) is PP and at least 80% of PP is
 CC approximately of the same molecular weight. Also described: (1) a
 CC recombinant fusion protein (I) comprising a polyanionic polypeptide and
 CC another polypeptide at either one end or at both ends of; (2) a

CC polyanionic polymer (II) conjugate comprising a polyanionic polymer and
 CC leukine, where the polyanionic polymer is polyglutamic acid or
 CC polyaspartic acid; (3) a vector (III) comprising a cassette which
 CC comprises a nucleotide sequence encoding a polyanionic polymer and at
 CC least one other nucleotide sequence, where the polyanionic polymer is
 CC polyglutamic acid or polyaspartic acid; (4) production of (I); (5) a cell
 CC comprising (III) or a vector that comprises a nucleotide sequence
 CC that encodes a polyanionic polymer that is larger than 10 kDa; and (6) a
 CC recombinantly-produced polyanionic polymer (V) that is of any molecular
 CC weight or is larger than 10 kD, and is conjugated to another protein. (I)
 CC is useful for treating a disease or ailment in an individual by
 CC administering (I) to the individual. (I) is also useful for delivering an
 CC effective amount of a pharmaceutically active agent, a therapeutic
 CC protein or a drug to a patient in need of it, or for diagnostic and
 CC testing or research purposes. ABZ22045 to ABZ22131 and ABP56374 to
 CC ABP56400 represent sequences used in the exemplification of the present
 CC invention

XX Sequence 19 AA;

Query Match 38.6%; Score 44; DB 6; Length 19;
 Best Local Similarity 57.1%; Pred. No. 34;
 Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 KIPEEKREKLEQ 22
 |||||
 Db 2 KMPEEEEEEEEE 15

RESULT 3

AA59156

ID AAB59156 standard; peptide; 20 AA.

XX AAB59156;

XX 21-MAR-2001 (first entry)

XX Alpha IIB beta 3 binding motif peptide #10.

XX Heptad repeat; transmembrane domain; cytoplasmic; integrin; inflammation;
 KW thrombosis; malignancy.
 XX Synthetic.
 XX WO200073341-A1.
 XX 07-DEC-2000.

XX 26-MAY-2000; 2000WO-US014656.

XX 27-MAY-1999; 99US-00320907.

XX (SCRI) SCRIPPS RES INST.

XX Ginsberg MH, Pfaff M;

XX WPI; 2001-041143/05.

XX Polypeptides useful in construction of structural models for identifying
 PT therapeutic compounds, comprises series of heptad repeats that mimic a
 PT transmembrane domain and cytoplasmic domain attached to the repeats.
 XX Disclosure; Page 13; 36pp; English.
 XX The present invention relates to a peptide with a series of heptad-
 CC repeats that mimic a transmembrane domain and a selected cytoplasmic
 CC domain attached to the heptad repeats. The invention is useful for
 CC evaluating structure and activity of a selected occupied and clustered
 CC transmembrane protein with the selected cytoplasmic domain and for
 CC identifying therapeutic compounds. It is also useful for identifying a
 CC cytoplasmic domain binding partner. It is also useful for identifying
 CC interactions with transmembrane proteins such as integrin, which can be
 CC used to treat conditions in which over activity of integrins is involved,

XX 09-OCT-1997; 97WO-US018331.
 XX
 PR 15-OCT-1996; 96US-0028420P.
 XX
 PA (UYVA-) UNIV VANDERBILT.
 XX
 PI Hawiger JJ, Timmons S, Liu X;
 XX WPI; 1998-251051/22.
 DR
 XX Inhibiting cellular adhesion useful e.g. to prevent tumour growth - by
 PT introducing peptide(s) comprising cell adhesion regulatory domain of an
 PT adhesion receptor or counter receptor sub-unit expressed by the cell.
 XX
 XX Example; Page 23; 76pp; English.
 XX This is the amino acid sequence of a peptide from human integrin beta-3-
 CC subunit, which is used in the method of the invention. This method
 CC involves the inhibition of cellular adhesion, with the use of peptides
 CC comprising a cell adhesion regulatory domain (CARD) of an adhesion
 CC receptor or counter receptor subunit expressed by the cell. The method is
 CC useful in treatments requiring inhibition of cellular adhesion e.g. to
 CC prevent growth of tumours, since adhesion is required to form tumour
 CC masses. It can be used to inhibit cellular inflammatory responses,
 CC (especially when the CARD is an integrin beta or alpha subunit), and to
 CC treat excessive fibroblast proliferation (especially to heal wounds) when
 CC the peptide comprises an integrin beta 1 CARD. The method is useful to
 CC treat coronary and/or vascular diseases, as well as respiratory distress
 CC syndrome, and retinosis in the blood
 XX
 SQ Sequence 19 AA;
 Query Match 36.8%; Score 42; DB 2; Length 19;
 Best Local Similarity 47.4%; Pred. No. 65;
 Matches 9; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 QY 1 KLGFFAHKIKPIEEKREEK 19
 Db 1 KAGFFKXNRPLSEDDDEE 19
 RESULT 7
 ADA27160
 ID ADA27160 standard; peptide; 7 AA.
 AC ADA27160;
 XX
 DT 20-NOV-2003 (first entry)
 XX Human integrin 10alpha subunit cytoplasmic domain motif.
 XX cytosolic; antiinflammatory; immunomodulator; neuroprotective;
 KW hemostatic; gene therapy; cancer; inflammation; immune disorder;
 KW neurological disorder; blood clotting disorder; food additive;
 KW preservative; secreted protein; integrin alpha; human.
 XX
 OS Homo sapiens.
 XX
 PN US2003055231-A1.
 XX
 PD 20-MAR-2003.
 XX
 PF 29-OCT-2001; 2001US-00984130.
 XX
 PR 28-OCT-1998; 98US-0105971P.
 PR 27-OCT-1999; 99WO-US025031.
 PR 19-APR-2000; 2000US-0198407P.
 PR 30-OCT-2000; 2000US-0243792P.
 PR 18-APR-2001; 2001US-00836353.
 XX
 XX (NIJ//) NI J.
 PA (YOUN//) YOUNG P E.

PA (KENN//) KENNY J J.
 PA (OLSE//) OLSEN H S.
 PA (MOOR//) MOORE P A.
 PA (WEIY//) WEI Y.
 PA (GREE//) GREENE J M.
 PA (RUBE//) RUBEN S M.
 PA (LIUD//) LIU D.
 PA (CROC//) CROCKER P R.
 XX
 PI Ni J, Young PE, Kenny JJ, Olsen HS, Moore PA, Wei Y, Greene JM;
 PI Ruben SM, Liu D, Crocker PR;
 XX WPI; 2003-567103/53.
 DR
 XX New human secreted nucleic acid molecules and polypeptides, useful for
 PT preventing, treating, or ameliorating a medical condition, such as
 PT cancer, inflammation, immune disorders, neurological and blood clotting
 PT disorders.
 XX
 XX Example 53; Page 257; 454pp; English.
 XX The invention relates to an isolated nucleic molecule that is at least
 CC 9% identical to 18 human cDNA sequences representing 12 novel genes
 CC encoding secreted proteins or a polynucleotide fragment of the cDNA
 CC sequence contained in American Type Culture Collection (ATCC) deposit No.
 CC defined in the specification, its species homologue, a variant or allelic
 CC variant of the polynucleotide having a polynucleotide capable of
 CC hybridising under conditions the polynucleotide, where the polynucleotide
 CC does not hybridise under stringent conditions to a nucleic acid molecule
 CC having a nucleotide sequence of only A or T residues. Also included are
 CC recombinant vectors, host cells (for producing the polypeptide), the
 CC secreted polypeptide (comprising a sequence that is at least 95%
 CC identical to a polypeptide fragment, domain, epitope, full-length
 CC protein, variant, allelic variant or species homologue), antibodies that
 CC specifically bind to the polypeptides, diagnosing, treating, preventing
 CC or ameliorating a medical condition by administering the polynucleotide
 CC or the polypeptide, the gene corresponding to the cDNA sequence and
 CC identifying an activity in a biological assay (by expressing the cDNA
 CC sequence in a cell, isolating the supernatant, and detecting an activity
 CC in a biological assay and identifying the protein in the supernatant
 CC having the activity). The polypeptides, nucleic acids and antibodies are
 CC useful for diagnosing a pathological condition or a susceptibility to a
 CC pathological condition, for preventing, treating, or ameliorating a
 CC medical condition, such as cancer, inflammation and other immune
 CC disorders, neurological and blood clotting disorders (many examples are
 CC given in the specification). The nucleic acids are also useful for
 CC chromosome identification, radiation hybrid mapping or long-range
 CC restriction mapping. The polypeptides and antibodies are useful for
 CC providing immunological probes for differential identification of the
 CC tissues immunohistochemistry assays. The polypeptide, polynucleotide,
 CC agonist or antagonist may also be used as a food additive or preservative
 CC to increase or decrease storage capabilities, fat content or other
 CC nutritional components. Novel gene 7 has been identified as encoding
 CC integrin alpha 11 subunit. The present sequence is the integrin alpha
 CC subunit conserved cytoplasmic domain motif as found in the gene7 protein
 CC or its homologue.
 XX
 SQ Sequence 7 AA;
 Query Match 34.2%; Score 39; DB 6; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLGFFAH 7
 Db 1 KLGFFAH 7
 RESULT 8
 ADI39445
 ID ADI39445 standard; peptide; 7 AA.
 XX
 AC ADI39445;

XX DT 22-APR-2004 (first entry)
 XX DE Integrin alpha10 cytoplasmic domain peptide sequence.
 XX KW MSC; mesenchymal stem cell; integrin alpha10; integrin alpha11;
 XX KW cell therapy; tissue repair; cytoplasmic domain.
 XX OS Unidentified.
 XX FN WO2003106492-A1.
 XX PD 24-DEC-2003.
 XX PF 12-JUN-2003; 2003WO-SE000983.
 XX PR 14-JUN-2002; 2002SE-00001831.
 XX PR 14-JUN-2002; 2002US-0388298P.
 XX PA (CART-) CARTELA AB.
 XX PI Lundgren-Akerlund E;
 XX DR WPI; 2004-062518/06.
 XX PT Marker for mammalian mesenchymal stem cells, useful for identifying and
 PT isolating mesenchymal stem cells, comprising integrin alpha 10 and/or
 PT integrin alpha 11 chain expressed on surface or within the stem cell.
 XX PS Disclosure; Page 2; 37pp; English.
 XX CC The invention relates to a marker (I) for mammalian mesenchymal stem
 CC cells (MSC), comprising an integrin alpha10 and/or integrin alpha11 chain
 CC expressed on cell surface of a MSC or intracellular in a MSC. (I) is
 CC useful for identification of a mammalian MSC, for modulating
 CC differentiation of a mammalian MSC and for isolating a mammalian MSC. (I)
 CC is useful for identifying, differentiating and isolating mammalian MSC
 CC from a mixed cell population as useful tools in cell therapy or in repair
 CC of damage tissue. The present sequence represents a sequence from the
 CC integrin alpha10 cytoplasmic domain which is present in the place of a
 CC conserved integrin cytoplasmic domain motif (ADI39444).
 XX SQ Sequence 7 AA;
 Query Match 34.2%; Score 39; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KLGFFAH 7
 Db 1 KLGFFAH 7
 RESULT 9
 ABP94377
 ID ABP94377 standard; peptide; 15 AA.
 AC ABP94377;
 XX DT 28-MAR-2003 (first entry)
 XX DE HLA protein 121P2A3 peptide #10732.
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX OS Homo sapiens.
 XX FN WO200283068-A2.
 XX PD 24-OCT-2002.
 XX PF 09-APR-2002; 2002WO-US011359.
 XX PR 10-APR-2001; 2001US-0282739P.
 XX PR 25-APR-2001; 2001US-0286630P.

PF 09-APR-2002; 2002WO-US011359.
 XX 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0286630P.
 PR 22-JUN-2001; 2001US-0300373P.
 XX (AGEN-) AGENSYS INC.
 XX Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI; 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 263; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene products
 CC in normal versus cancerous tissues. The proteins are useful for
 CC generating and characterising domain-specific antibodies, for identifying
 CC agents or cellular factors that bind to 121P2A3 or a particular structure
 CC domain, and in various therapeutic and diagnostic contexts, including
 CC cancer vaccines. The antibodies or T cells reactive with the product are
 CC useful in passive or active immunisation, and in imaging methodologies
 CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
 CC represent peptides from the 121P2A3 variants of the invention
 XX SQ Sequence 15 AA;
 Query Match 34.2%; Score 39; DB 6; Length 15;
 Best Local Similarity 53.3%; Pred. No. 1.4e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 AHKKIPEEKREKL 20
 Db 1 ARGKLEBEKKRSEEL 15
 RESULT 10
 ABP93904
 ID ABP93904 standard; peptide; 15 AA.
 AC ABP93904;
 XX DT 28-MAR-2003 (first entry)
 XX DE HLA protein 121P2A3 peptide #10259.
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX OS Homo sapiens.
 XX FN WO200283068-A2.
 XX PD 24-OCT-2002.
 XX PF 09-APR-2002; 2002WO-US011359.
 XX PR 10-APR-2001; 2001US-0282739P.
 XX PR 25-APR-2001; 2001US-0286630P.

PR 22-JUN-2001; 2001US-0300373P.
 XX (AGEN-) AGENSYS INC.
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI; 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 254; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene products
 CC in normal versus cancerous tissues. The proteins are useful for
 CC generating and characterising domain-specific antibodies, for identifying
 CC agents or cellular factors that bind to 121P2A3 or a particular structure
 CC domain, and in various therapeutic and diagnostic contexts, including
 CC cancer vaccines. The antibodies or T cells reactive with the product are
 CC useful in passive or active immunisation, and in imaging methodologies
 CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
 CC represent peptides from the 121P2A3 variants of the invention
 XX Sequence 15 AA;

Query Match 34.2%; Score 39; DB 6; Length 15;
 Best Local Similarity 53.3%; Pred. No. 1.4e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 AHKKIPEEEKREKL 20
 DB 1 ARGKLEEEKKRSSEL 15
 | | | | | | | |
 | | | | | | | |

RESULT 11
 ABP94921
 ID ABP94921 standard; peptide; 15 AA.
 XX
 AC ABP94921;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #11276.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 XX WO200283068-A2.
 XX
 XX 24-OCT-2002.
 XX
 XX 09-APR-2002; 2002WO-US011359.
 XX
 XX 10-APR-2001; 2001US-0282739P.
 XX 25-APR-2001; 2001US-0286630P.
 XX 22-JUN-2001; 2001US-0300373P.
 XX (AGEN-) AGENSYS INC.

PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI; 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 274; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene products
 CC in normal versus cancerous tissues. The proteins are useful for
 CC generating and characterising domain-specific antibodies, for identifying
 CC agents or cellular factors that bind to 121P2A3 or a particular structure
 CC domain, and in various therapeutic and diagnostic contexts, including
 CC cancer vaccines. The antibodies or T cells reactive with the product are
 CC useful in passive or active immunisation, and in imaging methodologies
 CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
 CC represent peptides from the 121P2A3 variants of the invention
 XX Sequence 15 AA;

Query Match 34.2%; Score 39; DB 6; Length 15;
 Best Local Similarity 53.3%; Pred. No. 1.4e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 AHKKIPEEEKREKL 20
 DB 1 ARGKLEEEKKRSSEL 15
 | | | | | | | |
 | | | | | | | |

RESULT 12
 ABP95230
 ID ABP95230 standard; peptide; 15 AA.
 XX
 AC ABP95230;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #11585.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 XX WO200283068-A2.
 XX
 XX 24-OCT-2002.
 XX
 XX 09-APR-2002; 2002WO-US011359.
 XX
 XX 10-APR-2001; 2001US-0282739P.
 XX 25-APR-2001; 2001US-0286630P.
 XX 22-JUN-2001; 2001US-0300373P.
 XX (AGEN-) AGENSYS INC.

PA Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI; 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 274; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene products
 CC in normal versus cancerous tissues. The proteins are useful for
 CC generating and characterising domain-specific antibodies, for identifying
 CC agents or cellular factors that bind to 121P2A3 or a particular structure
 CC domain, and in various therapeutic and diagnostic contexts, including
 CC cancer vaccines. The antibodies or T cells reactive with the product are
 CC useful in passive or active immunisation, and in imaging methodologies
 CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
 CC represent peptides from the 121P2A3 variants of the invention
 XX Sequence 15 AA;

QY 6 AHKKIPEEEKREKL 20
 DB 1 ARGKLEEEKKRSSEL 15
 | | | | | | | |
 | | | | | | | |

RESULT 12
 ABP95230
 ID ABP95230 standard; peptide; 15 AA.
 XX
 AC ABP95230;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #11585.
 XX
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 XX WO200283068-A2.
 XX
 XX 24-OCT-2002.
 XX
 XX 09-APR-2002; 2002WO-US011359.
 XX
 XX 10-APR-2001; 2001US-0282739P.
 XX 25-APR-2001; 2001US-0286630P.
 XX 22-JUN-2001; 2001US-0300373P.
 XX (AGEN-) AGENSYS INC.

XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX
 PS Claim 13; Page 280; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene products
 CC in normal versus cancerous tissues. The proteins are useful for
 CC generating and characterising domain-specific antibodies, for identifying
 CC agents or cellular factors that bind to 121P2A3 or a particular structure
 CC domain, and in various therapeutic and diagnostic contexts, including
 CC cancer vaccines. The antibodies or T cells reactive with the product are
 CC useful in passive or active immunisation, and in imaging methodologies
 CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
 CC represent peptides from the 121P2A3 variants of the invention
 XX
 SQ Sequence 15 AA;

Query Match 34.2%; Score 39; DB 6; Length 15;
 Best Local Similarity 53.3%; Pred. No. 1.4e+02;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 6 AHKKIPEEKREKL 20
 | | | | | | | | | |
 Db 1 ARGKLEEEKRSEEL 15

RESULT 13
 AAU85587
 ID AAU85587 standard; peptide; 20 AA.

XX AAU85587;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Lung tumour protein L548S peptide #22.
 XX
 KW Lung tumour; cancer; T cell; immune response stimulator; cytostatic.
 XX
 OS Homo sapiens.

XX WO200204514-A2.
 XX
 PD 17-JAN-2002.

XX 10-JUL-2001; 2001WO-US022058.
 XX
 PR 11-JUL-2000; 2000US-00614124.
 PR 29-AUG-2000; 2000US-00651563.
 PR 08-SEP-2000; 2000US-00658824.
 PR 26-SEP-2000; 2000US-00671325.
 PR 06-OCT-2000; 2000US-00677419.
 PR 30-OCT-2000; 2000US-00702705.
 PR 13-DEC-2000; 2000US-00736457.
 PR 03-MAY-2001; 2001US-00849626.

XX (CORI-) CORIXA CORP.
 XX
 PI Wang T, Watanabe Y, Henderson RA, Johnson JC, Retter MW;
 PI Marxakakis M, Carter D, Fanger GR, Vedvick TS, Bangur CS, Mcnabb A;
 PI Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
 XX
 DR WPI; 2002-164634/21.

XX Novel polynucleotide encoding a lung tumor polypeptide useful for
 PT stimulating and/or expanding T cells specific for a tumor protein.
 XX
 PS Claim 2; SEQ ID NO 1855; 223pp; English.
 XX
 CC The invention describes an isolated polynucleotide and polypeptide useful
 CC for stimulating and/or expanding T cells specific for a tumor protein
 CC for determining the presence of a cancer in a patient. A composition
 CC containing the polynucleotide and/or polypeptide is useful for treating a
 CC lung cancer in a patient. The polypeptide is useful for removing tumour
 CC cells from a biological sample. The polynucleotide is also useful as
 CC probe or primer to detect the level of mRNA encoding a tumour protein.
 CC This is the amino acid sequence of a lung tumour associated peptide,
 CC described in the method of the invention. Note: the sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 20 AA;

Query Match 34.2%; Score 39; DB 5; Length 20;
 Best Local Similarity 53.8%; Pred. No. 1.8e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AHKKIPEEKREE 18
 | | | | | | | | | |
 Db 8 ARKKVEEDEEE 20

RESULT 14
 ABU69559
 ID ABU69559 standard; peptide; 20 AA.

XX ABU69559;
 XX
 DT 05-JUN-2003 (first entry)
 XX
 DE Human lung cancer protein L548S CD4 epitope scanning peptide #22.
 XX
 KW Human; lung cancer; lung tumour; cytostatic; vaccine; T cell expansion;
 KW CD4; CD8; L548S; epitope.
 XX
 OS Homo sapiens.

XX US2002197669-A1.

PD 26-DEC-2002.

PF 03-MAY-2001; 2001US-00849626.

XX 13-DEC-2000; 2000US-00736457.

XX (BANG/) BANGUR C S.
 XX (FANG/) FANGER G R.
 XX (WANG/) WANG A.
 XX (WANG/) WANG T.
 XX (SWIT/) SWITZER A P.
 XX (MCNE/) MCNEILL P D.
 XX (CLAP/) CLAPPER J D.

XX Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;
 PI Clapper JD;

XX WPI; 2003-352750/33.

XX Novel lung cancer polynucleotide encoding lung cancer protein, useful for
 PT detecting the presence of lung cancer in a patient, and in pharmaceutical
 PT compositions, e.g. vaccines, for treating lung cancer.
 XX
 PS Example 6; Page; 72pp; English.

XX The invention relates to a polynucleotide encoding a lung tumour protein,

comprising a sequence selected from any of the 14 sequences mentioned in the specification, or a sequence (S2) mentioned in specification, complement of S1, sequences consisting of at least 20 contiguous residues of S1, sequences that hybridise to S1, sequences having 75%, preferably 90%, identity to S1, or degenerate variants of S1. Also included are an isolated polypeptide comprising a sequence (S3) selected from any one of the 4 amino acid sequences mentioned in the specification, a sequence encoded by the polynucleotide, or sequences having at least 70%, preferably 90%, identity to a sequence encoded by the polynucleotide), an expression vector comprising the polynucleotide operably linked to an expression control sequence, a host cell transformed or transfected with the vector, an isolated antibody (or its antigen-binding fragment) that specifically binds to the polypeptide, detecting the presence of a cancer in a patient, a fusion protein comprising the polypeptide, an oligonucleotide that hybridises to S1 under moderately stringent conditions, stimulating and/or expanding T cells specific for a tumour protein (comprising contacting T cells with the polynucleotide, protein or antigen-presenting cells, under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells) and inhibiting the development of a cancer in a patient (by incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with the polynucleotide, protein or antigen presenting cells that express the polynucleotide, such that T cells proliferate, administering to the patient an effective amount of the proliferated T cells, and thus inhibiting the development of a cancer in the patient. The polynucleotide, protein and cells are useful in a composition for stimulating an immune response in a patient, and for treating a cancer in a patient (particularly lung cancer). The oligonucleotide is useful for determining the presence of a cancer in a patient. The protein and oligonucleotides are useful in pharmaceutical compositions, e.g. vaccines. The polynucleotide is also useful as a probe or primer for nucleic acid hybridisation, and in the design and preparation of ribozyme molecules for inhibiting expression of tumour polypeptides and proteins in tumour cells. An amplified portion of the polynucleotide is useful for isolating a full-length gene from a suitable library. The present sequence is an epitope mapping peptide derived from the cDNA L548S isolated from a library derived from lung tumour/cancer cells. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO at seqdata.uspto.gov/sequence.html?DocId=20020197669

SQ Sequence 20 AA;
Query Match 34.2%; Score 39; DB 6; Length 20;
Best Local Similarity 53.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AHKKIPPEEKREE 18
Db 8 ARKKVEEEDDEEE 20
| | | : | | : | |
| | | : | | : | |

RESULT 15
ABU66462
ID ABU66462 standard; protein; 20 AA.

AC ABU66462;

DT 22-MAY-2003 (first entry)

XX Lung cancer therapy and diagnosis associated protein #86.

XX Lung cancer; cytostatic; vaccine; gene therapy; cancer.

XX Homo sapiens.

XX US200217952-A1.

XX 21-NOV-2002.

XX 10-JUL-2001; 2001US-00902941.

XX 30-JUN-1999; 99US-00346492.

PR 15-OCT-1999; 99US-00419356.

PR 17-DEC-1999; 99US-00466867.
PR 30-DEC-1999; 99US-00476300.
PR 06-MAR-2000; 2000US-00519642.
PR 22-MAR-2000; 2000US-00533077.
PR 10-APR-2000; 2000US-00546259.
PR 27-APR-2000; 2000US-00560406.
PR 05-JUN-2000; 2000US-00589184.
PR 11-JUL-2000; 2000US-00614124.
PR 29-AUG-2000; 2000US-00651563.
PR 08-SEP-2000; 2000US-00658824.
PR 28-SEP-2000; 2000US-00671325.
PR 06-OCT-2000; 2000US-00677419.
PR 30-OCT-2000; 2000US-00702705.
PR 13-DEC-2000; 2000US-00736457.
PR 03-MAY-2001; 2001US-00849626.
XX (CORI-) CORIXA CORP.
PA Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW;
XX Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;
PI WPI; 2003-328427/31.
XX

PT New polynucleotide, useful for preparing a composition for treating or inhibiting development of cancer, e.g. lung cancer.

PS Example 6; SEQID NO 1856; 82pp; English.

XX The invention describes an isolated polynucleotide comprising one of 32 sequences, complement or degenerate variants of them. The polynucleotide is useful for preparing a composition e.g. a vaccine or for gene therapy, for treating or inhibiting development of cancer, e.g. lung cancer. This sequence represents a polypeptide associated with the compositions and methods for the therapy and diagnosis of lung cancer

SQ Sequence 20 AA;

Query Match 34.2%; Score 39; DB 6; Length 20;
Best Local Similarity 53.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AHKKIPPEEKREE 18
Db 8 ARKKVEEEDDEEE 20
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Search completed: April 6, 2005, 14:58:46
Job time : 176 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 6, 2005, 14:58:57 ; Search time 138 Seconds
(without alignments)
52.927 Million cell updates/sec

Title: US-09-647-544-7

Perfect score: 114

Sequence: 1 KLGFPAHKIPEEKREKLEQ 22

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 33197259 residues

Total number of hits satisfying chosen parameters: 306921

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	44	38.6	19	13	US-10-101-487-67
2	44	38.6	20	9	US-09-320-907B-24
3	44	38.6	20	15	US-10-447-292-24
4	43	37.7	20	9	US-09-320-907B-15
5	43	37.7	20	15	US-10-447-292-15
6	42	36.8	16	16	US-10-786-505-26
7	39	34.2	20	9	US-09-736-457-1855
8	39	34.2	20	9	US-09-902-941-1855
9	39	34.2	20	9	US-09-849-626-1855
10	39	34.2	20	14	US-10-017-754-1855
11	39	34.2	20	14	US-10-113-872-1855
12	39	34.2	20	15	US-10-283-017-1855
13	38	33.3	22	9	US-09-864-761-36284

14	37	32.5	20	9	US-09-736-457-1856	Sequence 1856, Ap
15	37	32.5	20	9	US-09-902-941-1856	Sequence 1856, Ap
16	37	32.5	20	9	US-09-849-626-1856	Sequence 1856, Ap
17	37	32.5	20	14	US-10-017-754-1856	Sequence 1856, Ap
18	37	32.5	20	14	US-10-113-872-1856	Sequence 1856, Ap
19	37	32.5	20	15	US-10-283-017-1856	Sequence 1856, Ap
20	36	31.6	13	10	US-09-876-904A-510	Sequence 510, App
21	36	31.6	13	10	US-09-733-179A-5	Sequence 5, Appli
22	36	31.6	14	9	US-09-320-907B-17	Sequence 17, Appl
23	36	31.6	14	10	US-09-733-179A-15	Sequence 15, Appl
24	36	31.6	14	15	US-10-447-292-17	Sequence 17, Appl
25	36	31.6	16	9	US-09-320-907B-16	Sequence 16, Appl
26	36	31.6	16	10	US-09-733-179A-4	Sequence 4, Appli
27	36	31.6	16	15	US-10-447-292-16	Sequence 16, Appl
28	36	31.6	19	15	US-10-350-405-7	Sequence 7, Appli
29	36	31.6	19	15	US-10-324-143-118	Sequence 118, App
30	36	31.6	21	15	US-10-005-305-19	Sequence 19, Appl
31	36	31.6	21	17	US-10-950-010-101	Sequence 101, App
32	36	31.6	22	15	US-10-005-305-20	Sequence 20, Appl
33	36	31.6	22	17	US-10-350-010-100	Sequence 100, App
34	34	29.8	19	14	US-10-059-720-4	Sequence 4, Appli
35	34	29.8	20	9	US-09-880-149-1	Sequence 1, Appli
36	34	29.8	20	13	US-10-038-045-15	Sequence 15, Appl
37	34	29.8	20	14	US-10-177-550-21	Sequence 21, Appl
38	34	29.8	20	14	US-10-345-281-1	Sequence 1, Appli
39	34	29.8	21	14	US-10-057-789-231	Sequence 231, App
40	34	29.8	21	14	US-10-212-628-231	Sequence 231, App
41	34	29.8	21	14	US-10-177-550-5	Sequence 5, Appli
42	34	29.8	21	14	US-10-177-550-26	Sequence 26, Appl
43	34	29.8	21	14	US-09-320-907B-25	Sequence 25, Appl
44	33.5	29.4	15	15	US-10-447-292-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-101-487-67
; Sequence 67, Application US/10101487
; Publication No. US20020169125A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, DAVID W.
; APPLICANT: BERGMAN, PHILIP A.
; APPLICANT: LOFQUIST, ALAN
; APPLICANT: PIETZ, GREGORY E.
; APPLICANT: TOMPKINS, CHRISTOPHER K.
; APPLICANT: WAGGONER JR., DAVID W.
; TITLE OF INVENTION: RECOMBINANT PRODUCTION OF POLYANIONIC POLYMERS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 077319/0329
; CURRENT APPLICATION NUMBER: US/10101487
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: 60/277,705
; PRIOR FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-10-101-487-67

Query Match 38.6%; Score 44; DB 13; Length 19;
Best Local Similarity 57.1%; Pred. No. 40;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 KIPPEEKREKLEQ 22

|||||

Db 2 KMPPEEEEEEE 15

RESULT 8
US-09-902-941-1855
; Sequence 1855, Application US/09902941
; Patent No. US20030172952A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, TongTong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnerakis, Margarita

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RESULT 10
US-10-017-754-1855
; Sequence 1855, Application US/10017754
; Publication No. US20030054363A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongfong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Marnarakis, Margarita
; APPLICANT: Carter, Darrick

```

; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: McNabb, Andria
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.478C18
 ; CURRENT APPLICATION NUMBER: US/10/017,754
 ; CURRENT FILING DATE: 2001-10-29
 ; NUMBER OF SEQ ID NOS: 2004
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1855
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-017-754-1855

Query Match 34.2%; Score 39; DB 14; Length 20;
 Best Local Similarity 53.8%; Pred. No. 2e+02;
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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 Db 8 ARKKVEEDSEEE 20

RESULT 11
 US-10-113-872-1855
 ; Sequence 1855, Application US/10113872
 ; Publication No. US20030170255A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.478C19
 ; CURRENT APPLICATION NUMBER: US/10/113.872
 ; CURRENT FILING DATE: 2002-03-28
 ; NUMBER OF SEQ ID NOS: 2011
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1855
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-113-872-1855

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 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AHKKIPEEKREE 18
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 Db 8 ARKKVEEDSEEE 20

RESULT 12
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 ; Sequence 1855, Application US/10283017
 ; Publication No. US20030211510A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Sleath, Paul R.
 ; APPLICANT: Johnson, Jeffrey C.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Durham, Margarita

; APPLICANT: Carter, Darrick
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: McNabb, Andria
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.478C20
 ; CURRENT APPLICATION NUMBER: US/10/283,017
 ; CURRENT FILING DATE: 2002-10-28
 ; NUMBER OF SEQ ID NOS: 2157
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1855
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-283-017-1855

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Qy 6 AHKKIPEEKREE 18
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 Db 8 ARKKVEEDSEEE 20

RESULT 13
 US-09-864-761-36284
 ; Sequence 36284, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aeomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21

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; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 36284
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; ORGANISM: Homo sapiens
; FEATURE:
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; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.92
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US-09-864-761-36284

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; Patent No. US20020168637A1
; GENERAL INFORMATION:

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; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1856
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1856

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Query Match      32.5%; Score 37; DB 9; Length 20;
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Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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Db 2 KKVVEEDEEEEEE 16

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US-09-902-941-1856
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; Patent No. US20020172952A1
; GENERAL INFORMATION:

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; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.

```

```

; APPLICANT: Marnerakis, Margarita
; APPLICANT: Carter, Darrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C17
; CURRENT APPLICATION NUMBER: US/09/902,941
; CURRENT FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 2002
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1856
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-1856

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Query Match      32.5%; Score 37; DB 9; Length 20;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

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Db 2 KKVVEEDEEEEEE 16

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 14:50:40 ; Search time 43 Seconds
(without alignments)
38.193 Million cell updates/sec

Title: US-09-647-544-7

Perfect score: 114

Sequence: 1 KLGFFAHKKIPBEKREKLEQ 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 207443

Minimum DB seq length: 0

Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pap:*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pap:*

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5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap:*

6: /cgn2_6/ptodata/1/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	37.7	20	1	US-08-214-770-1
2	43	37.7	20	5	PCT-US95-02885-1
3	43	37.7	20	5	PCT-US95-07542-15
4	39	34.2	20	4	US-09-736-457-1855
5	39	34.2	20	6	5225193-7
6	39	34.2	20	6	5225193-7
7	37	32.5	20	4	US-09-736-457-1856
8	36	31.6	20	6	5225193-2
9	36	31.6	20	6	5225193-2
10	36	31.6	21	1	US-08-073-028-25
11	36	31.6	21	1	US-08-127-499A-15
12	36	31.6	21	1	US-08-482-847-15
13	36	31.6	21	3	US-08-554-616-25
14	36	31.6	21	4	US-09-515-965A-1640
15	36	31.6	21	4	US-09-350-841A-1669
16	36	31.6	21	4	US-10-005-305-19
17	36	31.6	22	1	US-08-073-028-24
18	36	31.6	22	3	US-08-554-616-24
19	36	31.6	22	4	US-09-515-965A-1641
20	36	31.6	22	4	US-09-350-841A-1670
21	36	31.6	22	4	US-10-005-305-20
22	35	30.7	21	5	PCT-US95-07542-11
23	34	29.8	13	1	US-08-056-200-11
24	34	29.8	13	1	US-07-987-272A-6
25	34	29.8	13	2	US-08-800-644-11
26	34	29.8	18	2	US-08-649-991-49
27	34	29.8	19	2	US-08-690-011A-4

28 34 29.8 19 3 US-09-299-495F-4 Sequence 4, Appli
29 34 29.8 20 1 US-08-199-776-21 Sequence 21, Appl
30 34 29.8 20 3 US-08-663-731-21 Sequence 21, Appl
31 34 29.8 20 3 US-08-879-338-21 Sequence 21, Appl
32 34 29.8 20 3 US-09-406-781-1 Sequence 1, Appli
33 34 29.8 20 4 US-09-181-941-15 Sequence 15, Appl
34 34 29.8 20 4 US-09-293-238B-21 Sequence 21, Appl
35 34 29.8 20 4 US-09-880-132-1 Sequence 1, Appli
36 34 29.8 20 5 PCT-US95-02044-21 Sequence 5, Appl
37 34 29.8 21 1 US-08-199-776-5 Sequence 5, Appl
38 34 29.8 21 1 US-08-555-579-1 Sequence 1, Appli
39 34 29.8 21 3 US-08-663-731-5 Sequence 5, Appli
40 34 29.8 21 3 US-08-879-338-5 Sequence 5, Appli
41 34 29.8 21 3 US-08-879-338-26 Sequence 26, Appl
42 34 29.8 21 4 US-09-293-238B-5 Sequence 5, Appl
43 34 29.8 21 4 US-09-293-238B-26 Sequence 26, Appl
44 34 29.8 21 5 PCT-US95-02044-5 Sequence 5, Appli
45 33.5 29.4 20 4 US-10-142-935-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-08-214-770-1
; Sequence 1, Application US/08214770
; Patent No. 5223209
; GENERAL INFORMATION:
; APPLICANT: Ginsberg, Mark H.
; APPLICANT: O'Toole, Tim
; TITLE OF INVENTION: METHODS FOR IDENTIFYING
; TITLE OF INVENTION: INHIBITORS OF INTEGRIN
; TITLE OF INVENTION: ACTIVATION
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,770
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06410/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-214-770-1

Query Match 37.7%; Score 43; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 9; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

5225193-7
Query Match 34.2%; Score 39; DB 6; Length 20;
Best Local Similarity 35.0%; Pred. No. 51;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 KLGFFFAHKKIPPEEKREKL 20
| : ||: || | : :
Db 1 KSEYLAHRRIPPENIRTRV 20
| : ||: || | : :
RESULT 6
5225193-7
; APPLICANT: BARTFAI, TAMAS
; TITLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/346,837
; FILING DATE: 19-OCT-1987
; SEQ ID NO:7:
; LENGTH: 20
5225193-7
Query Match 34.2%; Score 39; DB 6; Length 20;
Best Local Similarity 35.0%; Pred. No. 51;
Matches 7; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 KLGFFFAHKKIPPEEKREKL 20
| : ||: || | : :
Db 1 KSEYLAHRRIPPENIRTRV 20
| : ||: || | : :
RESULT 7
US-09-736-457-1856
; Sequence 1856, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1856
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1856
Query Match 32.5%; Score 37; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 95;
Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
QY 8 KKIPEEEKREKLEQ 22
| : ||: || | : :
Db 2 KKVEEDEEQEERE 16
| : ||: || | : :
RESULT 8
5225193-2
; Patent No. 5225193

; APPLICANT: BARTFAI, TAMAS
; TITLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/346,837
; FILING DATE: 19-OCT-1987
; SEQ ID NO:2:
; LENGTH: 20
5225193-2
Query Match 31.6%; Score 36; DB 6; Length 20;
Best Local Similarity 46.2%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 FFAHKKIPPEEK 16
| : ||: || | : :
Db 3 YLAHRRIPPENIR 15
| : ||: || | : :
RESULT 9
5225193-2
; Patent No. 5225193
; APPLICANT: BARTFAI, TAMAS
; TITLE OF INVENTION: BORDETELLA TOXIN PEPTIDES AND VACCINES
; NUMBER OF SEQUENCES: 10
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/346,837
; FILING DATE: 19-OCT-1987
; SEQ ID NO:2:
; LENGTH: 20
5225193-2
Query Match 31.6%; Score 36; DB 6; Length 20;
Best Local Similarity 46.2%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 4 FFAHKKIPPEEK 16
| : ||: || | : :
Db 3 YLAHRRIPPENIR 15
| : ||: || | : :
RESULT 10
US-08-073-028-25
; Sequence 25, Application US/08073028
; Patent No. 5464933
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; FILE REFERENCE: TRANSMISSION
; CURRENT APPLICATION NUMBER: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/073,028
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-004-999
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-073-028-25

Query Match 31.6%; Score 36; DB 1; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HKKIPPEEKREKLEQ 22
Db 6 HSLIESQNOQEKNEQ 21

RESULT 11

US-08-127-499A-15
; Sequence 15, Application US/08127499A
; Patent No. 5510264
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
; TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/127,499A
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/102/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-127-499A-15

Query Match 31.6%; Score 36; DB 1; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HKKIPPEEKREKLEQ 22
Db 1 HSLIESQNOQEKNEQ 16

RESULT 12

US-08-482-847-15
; Sequence 15, Application US/08482847

; Patent No. 5556757
; GENERAL INFORMATION:
; APPLICANT: VAN ALSTYNE, Diane
; APPLICANT: SHARMA, Lawrence Rajendra
; TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
; TITLE OF INVENTION: BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR
; TITLE OF INVENTION: CNS CARRIER, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,847
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,499
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 51916/104/INBI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-482-847-15

Query Match 31.6%; Score 36; DB 1; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HKKIPPEEKREKLEQ 22
Db 1 HSLIESQNOQEKNEQ 16

RESULT 13

US-08-554-616-25
; Sequence 25, Application US/08554616
; Patent No. 6133418
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; TITLE OF INVENTION: SYNTHETIC PEPTIDE INHIBITORS OF HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/554,616
FILING DATE: 06-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,028
FILING DATE: 07-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-004-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-554-616-25

Query Match 31.6%; Score 36; DB 3; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HKKIPEEEKREKLEQ 22
Db 6 HSLIEESQOQEKNEQ 21

RESULT 14

US-09-515-965A-1640
Sequence 1640, Application US/09515965A
Patent No. 6823741
GENERAL INFORMATION:
APPLICANT: Antczak, J.
APPLICANT: Delmedico, M.
APPLICANT: Erickson, J.
APPLICANT: Lambert, D.
APPLICANT: Sisca, P.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-
TITLE OF INVENTION: ASSOCIATED EVENTS INCLUDING RSV TRANSMISSION
FILE REFERENCE: 7872-073
CURRENT APPLICATION NUMBER: US/09/515,965A
CURRENT FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 09/315,304
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/082,279
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 1994
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1640
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Core polypeptide
US-09-515-965A-1640

Query Match 31.6%; Score 36; DB 4; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HKKIPEEEKREKLEQ 22
Db 6 HSLIEESQOQEKNEQ 21

RESULT 15

US-09-350-841A-1669
Sequence 1669, Application US/09350841A
Patent No. 6750008
GENERAL INFORMATION:
APPLICANT: Jeffes, Peter;
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
FILE REFERENCE: 7872-066-999
CURRENT APPLICATION NUMBER: US/09/350,841A
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 1946
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1669
LENGTH: 21
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: core polypeptide
US-09-350-841A-1669

Query Match 31.6%; Score 36; DB 4; Length 21;
Best Local Similarity 43.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 7 HKKIPEEEKREKLEQ 22
Db 6 HSLIEESQOQEKNEQ 21

Search completed: April 6, 2005, 15:00:24
Job time : 44 secs

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